



FIG. 1A

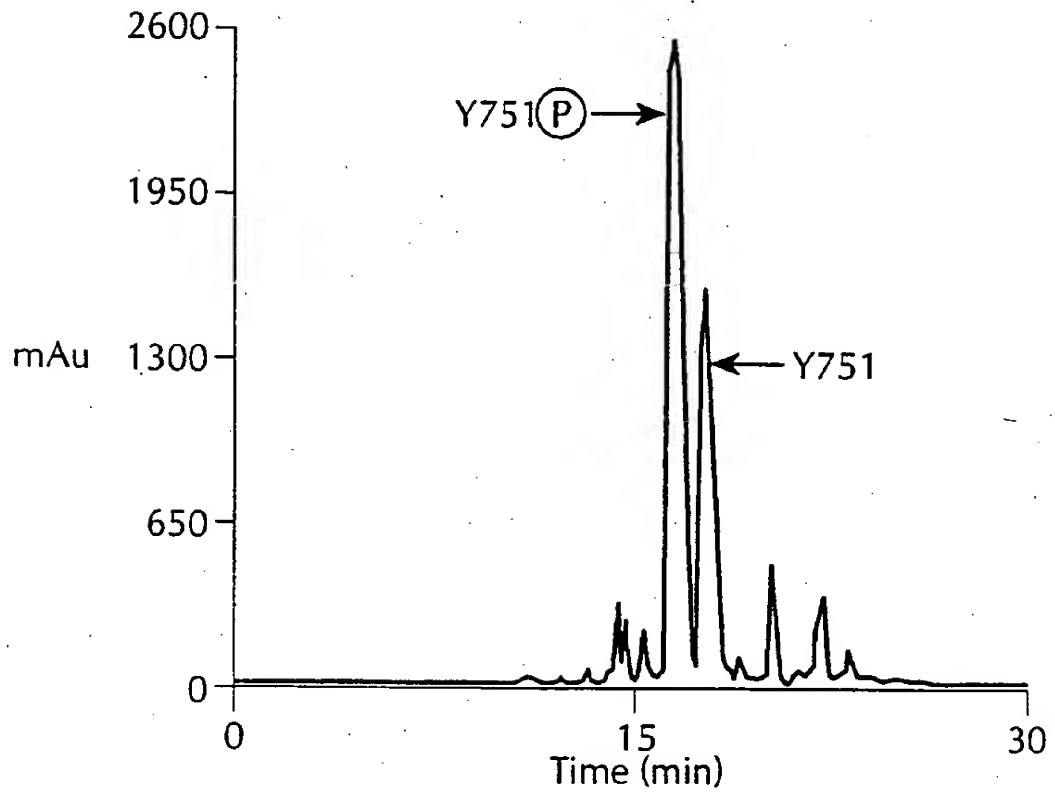
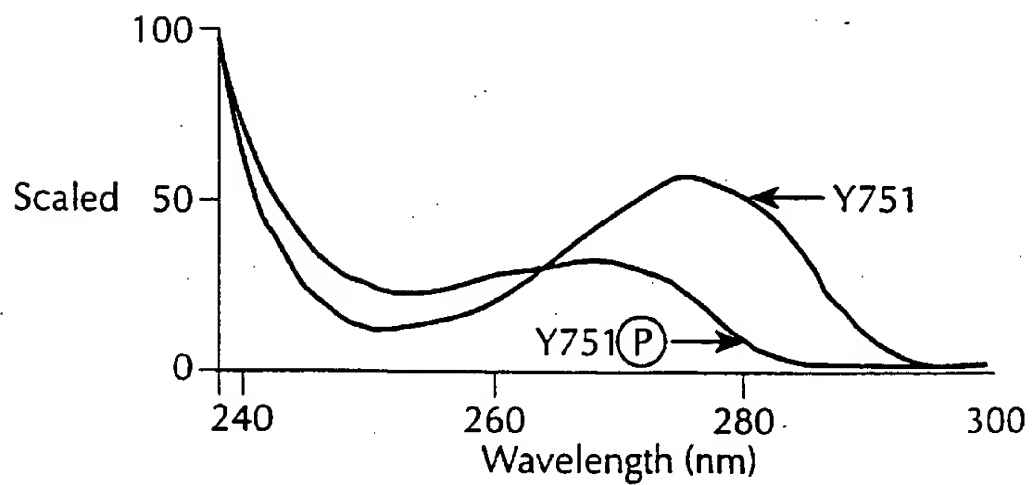


FIG. 1B



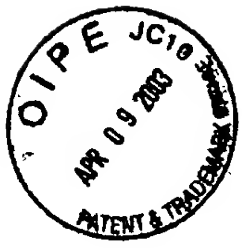


FIG. 1C

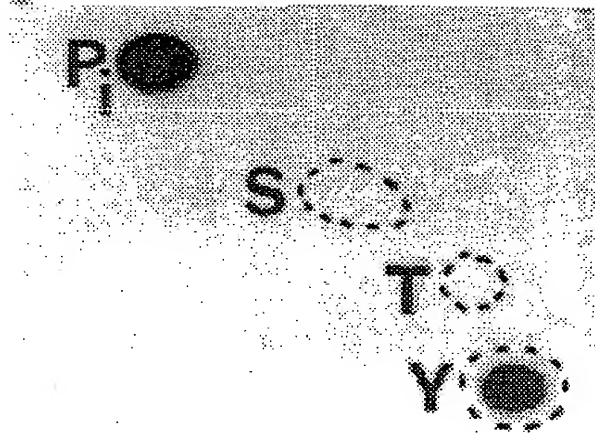
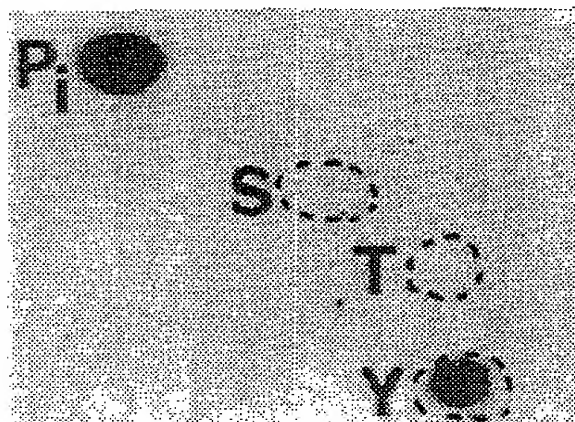


FIG. 1D



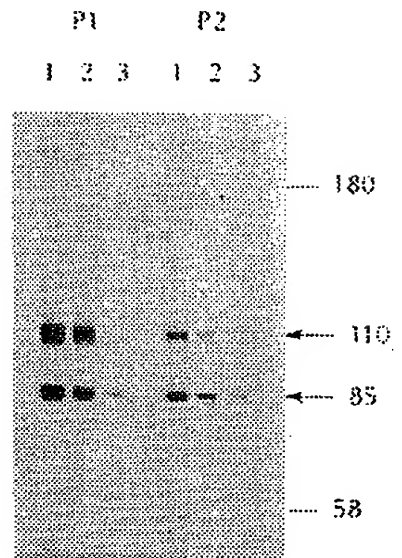




FIG. 3

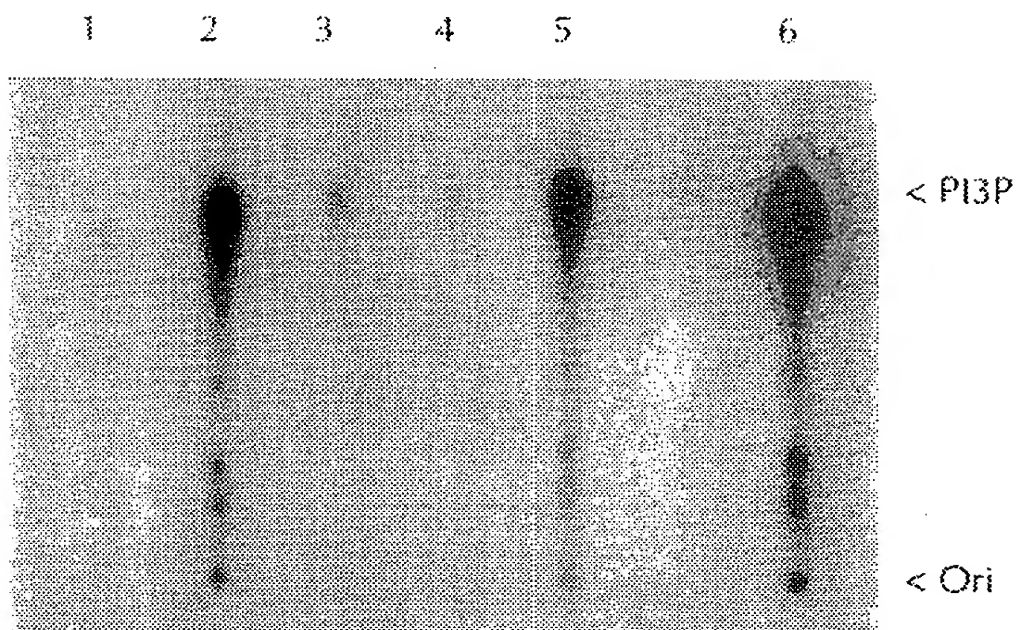
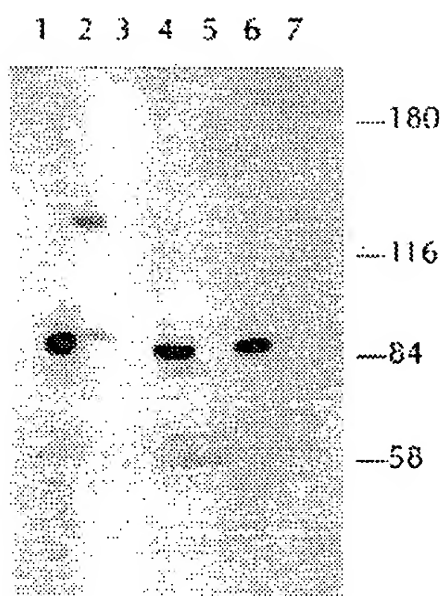


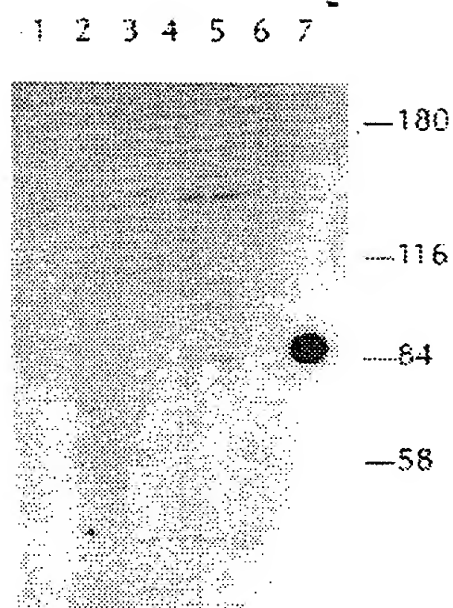


FIG. 4A

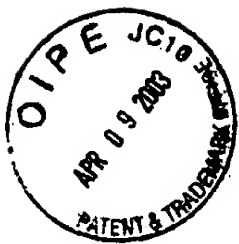


anti-ALPHA

FIG. 4B



anti-BETA



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EXCEPT BY AUTHORITY

FIG. 4C

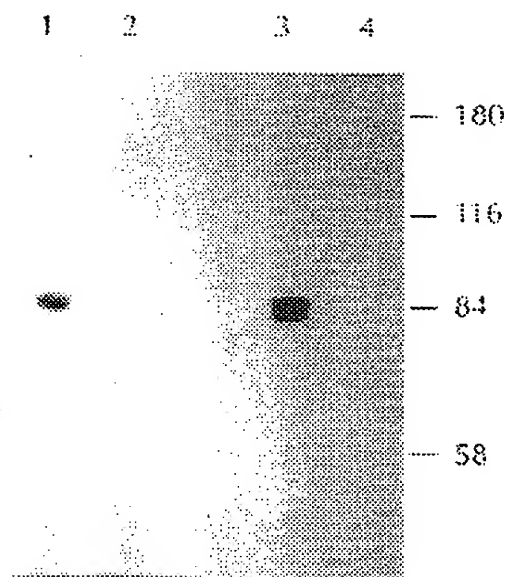


FIG. 4D

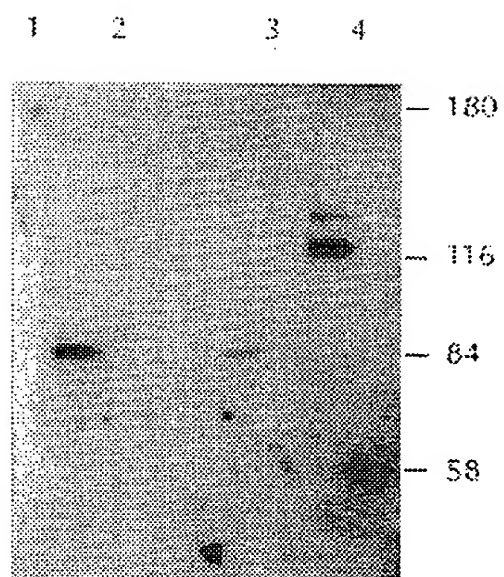




FIG. 5A

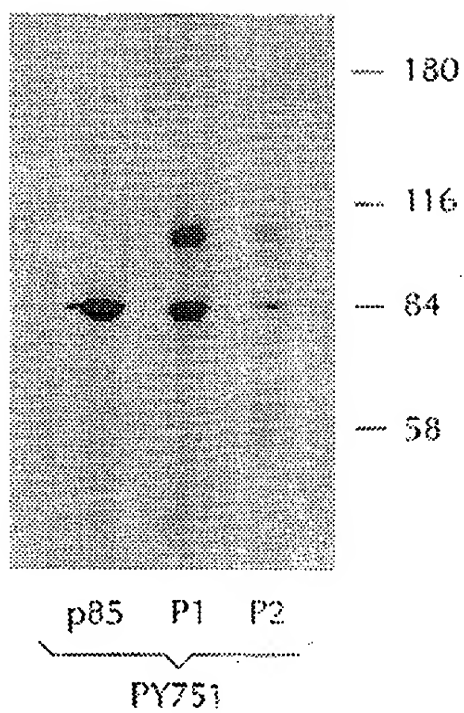


FIG. 5B

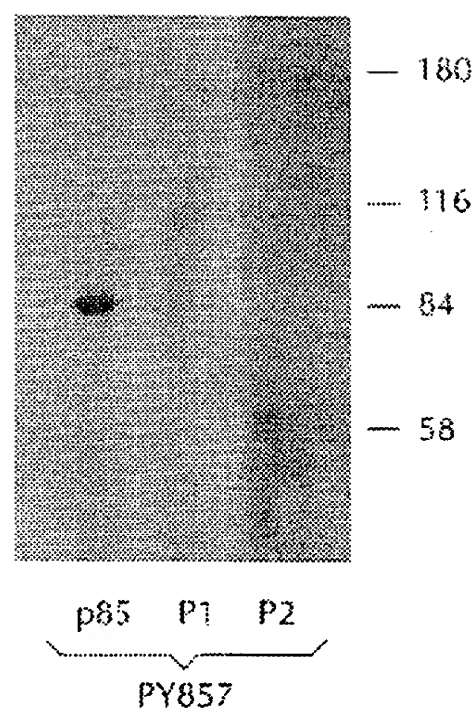




FIG. 6A

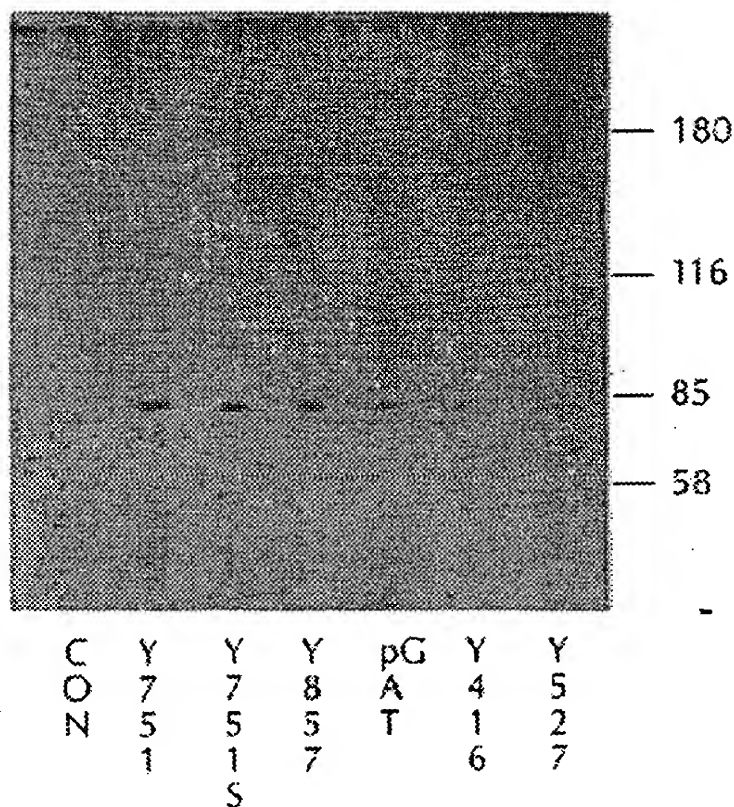
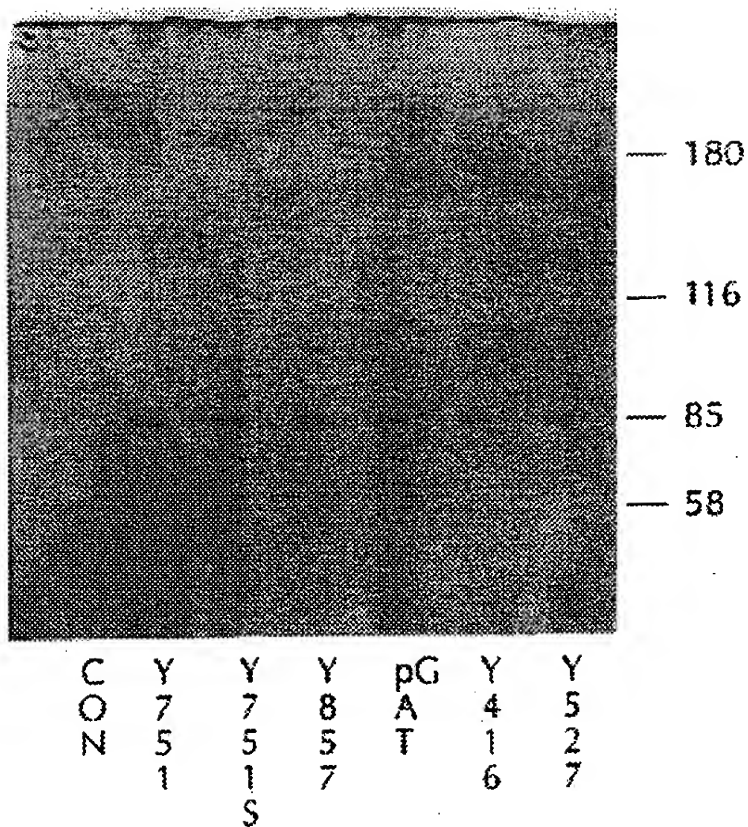


FIG. 6B



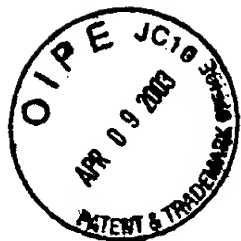


FIG. 7A

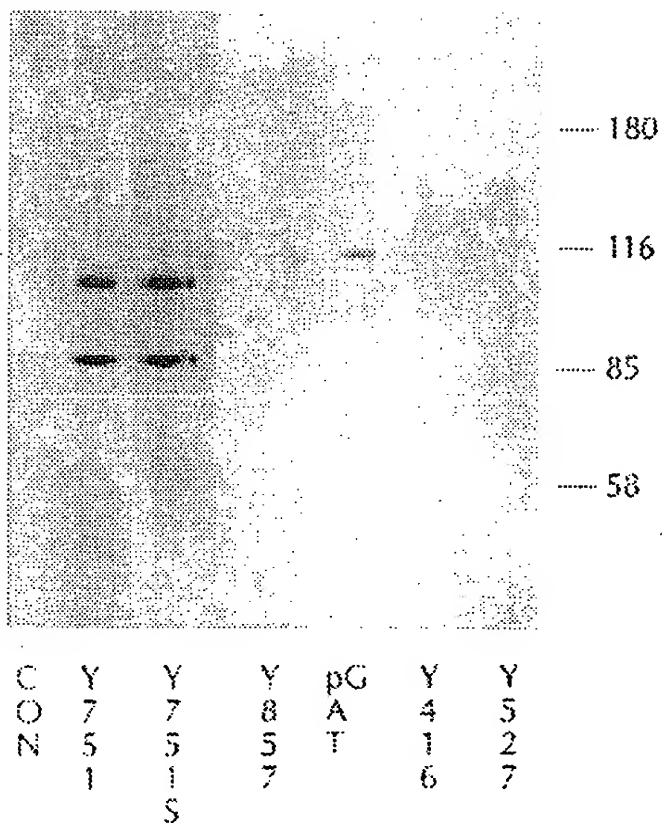


FIG. 7B

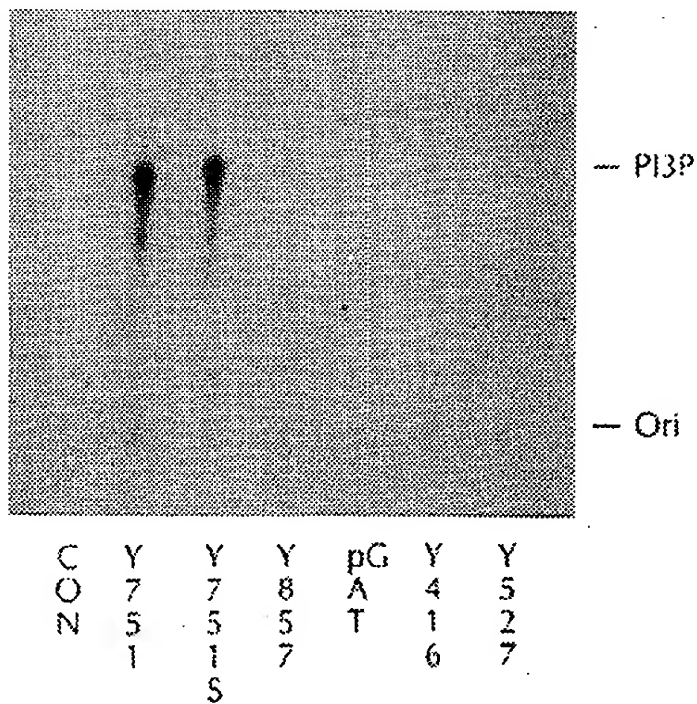




FIG. 8A

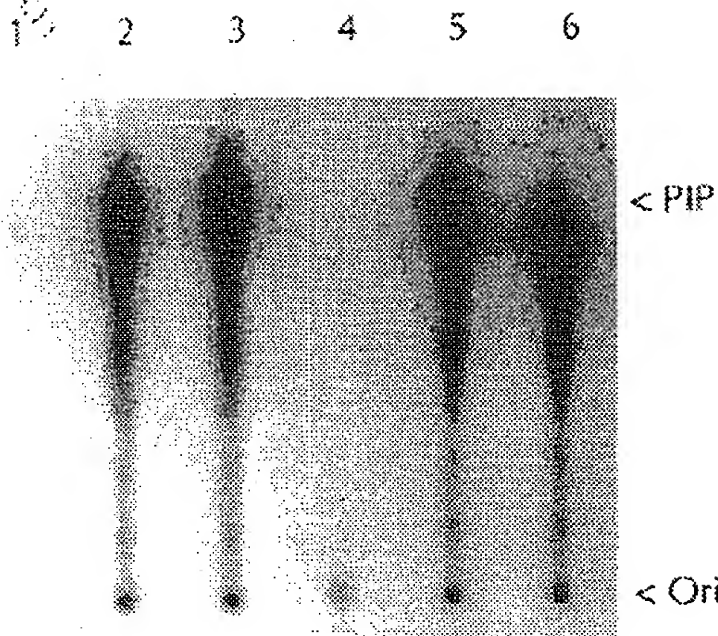


FIG. 8B

751	D M S K D E S V D Y V P M L D M K
751.S	C D E S V D Y V P M L
740	G E S D G G Y M D M S K
1313	E F C P D P L Y E V M L K
Consensus	E E E E E Y M P M X X
	D D D D D V



FIG. 9A

M P P R P S S G E L W G I H L M	16
ATGCCTCCAAGACCATCATCAGGTGAACTGTGGGGCATCCACTTGATG	48
P P R I L V E C L L P N G M I V	32
CCCCAAGAATCCTAGTAGAATGTTTACTACCAAATGGGATGATAGTG	96
T L E C L R E A T L I T I K H E	48
ACTTTAGAATGCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAA	144
L F K E A R K Y P L H Q L L Q D	64
CTATTTAAAGAAGCAAGAAAATACCCTCTCCATCAACTTCTTCAAGAT	192
E S S Y I F V S V T Q E A E R E	80
GAATCTTCTTACATTTTTCGTAAGTGTTACCCAAGAAGCAGAAAGGGAA	240
E F F D E T R R L C D L R L F Q	96
GAATTTTTTGTATGAAACAAGAAGACTTTGTGACCTTCGGCTTTTTTCAA	288
P F L K V I E P V G N R E E K I	112
CCCTTTTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAGAAAAGATC	336
L N R E I G F A I G M P V C E F	128
CTCAATCGAGAAATTGGTTTTGCTATCGGCATGCCAGTGTGTGAATTC	384
D M V K D P E V Q D F R R N I L	144
GATATGGTTAAAGATCCAGAAGTACAGGACTTCGAAGAAATATTCTC	432



FIG. 9B

N V C K E A V D L R D L N S P H 160
AATGTTTGTAAGAAGCTGTGGATCTTAGGGATCTTAATTCACCTCAT 480
A
S R A M Y V Y P P N V E S S P E - 176
AGTAGAGCAATGTATGTTTATCTCCAAATGTAGAATCTTCACCAGAA 528
L P K H I Y N K L D K G Q I I V 192
CTGCCAAAGCACATATATAATAAATTGGATAAAGGGCAAATAATAGTG 576
V I W V I V S P N N D K Q K Y T 208
GTGATTGTTGGTAATAGTTTCTCCAAATAATGACAAACAGAAGTATACT 624
L K I N H D C V P E Q V I A E A 224
CTGAAAATCAACCATGACTGTGTGCCAGAACAGTAATTGCTGAAGCA 672
I R K K T R S M L L S S E Q L K 240
ATCAGGAAAAAACTCGAAGTATGTTGCTATCATCTGAACAACTAAAA 720
L C V L E Y Q G K Y I L K V C G 256
CTCTGTGTTTLAGAATATCAGGGCAAGTATATTTTAAAAGTGTGTGGA 768
C D E Y F L E K Y P L S Q Y K Y 272
TGTGATGAATACTTCCTAGAAAAATATCCTCTGAGTCAGTATAAGTAT 816
I R S C I M L G R M P N L M L M 288
ATAAGAAGCTGTATAATGCTTGGGAGGATGCCCAATTTGATGCTGATG 864



FIG. 9D

T D T L V S G K M A L N L W P V 448
ACAGATACTCTAGTATCTGGAAAAATGGCTTTGAATCITTGGOCAGTA 1344
C
P H G L E D L L N P I G V T G S 464
CCTCATGGACTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCA 1392
N P N K E T P C L E L E F D W F 480
AATCCAAATAAAGAACTCCATGTTTAGAGTTGGAGTTTGAAGAGCATGCC 1440
S S V V K F P D M S V I E E H A 496
AGCAGTGTGGTAAAGTTTCCAGATATGTCAGTGATTGAAGAGCATGCC 1488
N W S V S R E A G F S Y S H A G 512
AATTGGTCTGTATCCCGTGAAGCAGGATTTAGTTATTCCCATGCAGGA 1536
L S N R L A R D N E L R E N D K 528
CTGAGTAACAGACTAGCTAGAGACAATGAATTAAGAGAAAATGATAAA 1584
E Q L R A I C T R D P L S E I T 544
GAACAGCTCOGAGCAATTTGTACACGAGATCCTCTATCTGAAATCACT 1632
E Q E K D F L W S H R H Y C V T 560
GAGCAAGAGAAAGATTTTCTGTGGAGCCACAGACACTATTGTGTAAGT 1680
I P E I L P K L L L S V K W N S 576
ATCCCCGAAATTCTACCCAAATTGCTTCTGTCTGTTAAATGGAAGTCT 1728



FIG. 9E

R D E V A Q M Y C L V K D W P P 592
AGAGATGAAGTAGCTCAGATGTACTGCTTGGTAAAAGATTGGCCTCCA 1776

I K P E Q A M E L L D C N Y P D 608
ATCAAGCCTGAACAGGCTATGGAGCTTCTGGACTGCAATTACCCAGAT 1824

P M V R G F A V R C L E K Y L T 624
CCTATGGITCGAGGTTTTGCTGTTGGTGCTTAGAAAAATATTTAACA 1872

D
D D K L S O Y L I O L V O V L K 640
GATGACAACTTTCTCAGTACCTAATTCAGCTAGTACAGGTACTAAAA 1920

Y E O Y L D N L L V R F L L K K 656
TATGAACAGTATTTGGATAACCTGCTTGTGAGATTTTACTCAAAAAA 1968

E
A L T N O R I G H F F F W H L K 672
GCGTTAACTAATCAAAGGATCGGTCACCTTTTCTTTTGGCATTAAAA 2016

F
S E M H N K T V S O R F G L L L 688
TCTGAGATGCACAATAAAACAGTTAGTCAGAGGTTTGGCCTGCTTTTG 2064

E S Y C R A C G M Y L K H L N R 704
GAGTCCTATTGCCGTGCATGTGGGATGTATCTGAAGCACCTTAATAGG 2112

G
Q V E A M E K L I N L T D I L K 720
CAAGTTGAGGCTATGGAAAAGCTCATTAACTTGACTGACATTCTCAAA 2160



FIG. 9F

Q E K K D E T Q K V Q M K F L V 736
CAAGAGAAGAAGGATGAAACACAAAAGGTACAGATGAAGTTTTTAGTT 2208

E Q M R R P D F M D A L Q G F L 752
GAGCAAATGCGGCGAACCAGATTTTCATGGATGCTCTCCAGGGCTTTCTG 2256

S P L N P A H Q L G N L R L E E 768
TCTCCTCTAAACCTGCTCATCAGCTGGGAAATCTCAGGCTTGAAGAG 2304

C R I M S S A K R P L W L N W E 784
TGTCGAATTATGTCTTCTGCAAAAAGGOCCTGTGGTTGAATTGGGAG 2352

N P D I M S E L L F Q N N E I I 800
AACCAGACATCATGTCAGAATTACTCTTTTCAGAACAAATGAGATCATC 2400

F K N G D D L R Q D M L T L Q I 816
TTTAAAAATGGGGATGATTTACGGCAAGATATGCTAACCCTTCAGATT 2448

I R I M E N I W Q N Q G L D L R 832
ATTGCAATTATGGAAAATATCTGGCAAAATCAAGGTCTTGATCTTOGA 2496

M L P Y G C L S I G D C V G L I 848
ATGTTAOCCTTATGGATGTCTGTCAATCGGTGACTGTGTGGGACTTATC 2544

E V V R N S H T I M Q I Q C K G 864
GAGGTGGTGAGAAATTCTCACACTATAATGCAGATTCACTGTAAAGGA 2592



FIG. 9H

Q H A N L F I N L F S M M L G S 1008
CAGCATGCCAATCTCTTCATAAATCTTTTCTCAATGATGCTTGGCTCT 3024

G M P E L Q S F D D I A Y I R K 1024
GGAATGCCAGAACTGCAATCTTTTGATGATATTGCATACATTGAAAG 3072

T L A L D K T E O E A L E Y F M 1040
ACCCTAGCTTTAGATAAACTGAGCAAGAGGCTTTGGAGTATTTTCATG 3120

K Q M N D A H H G G W T T K M D 1056
AAACAAATGAATGATGCACACCATGGTGGCTGGACAACAAAAATGGAT 3168

W I F H T I K Q H A L N * 1069
TGGATCTTCCACACAATTAAGCAGCATGCTTTGAACTGA 3207



FIG. 9I

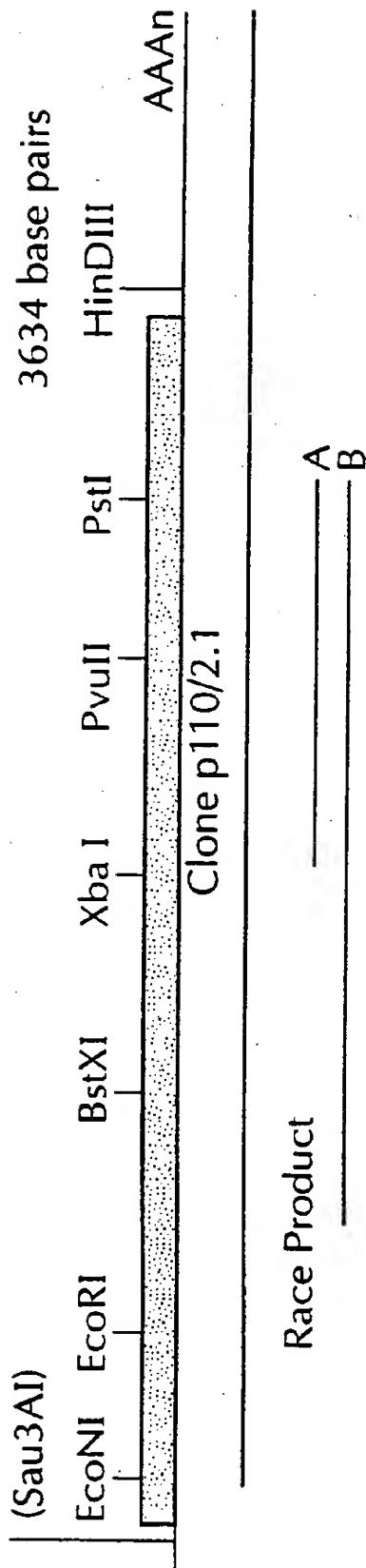
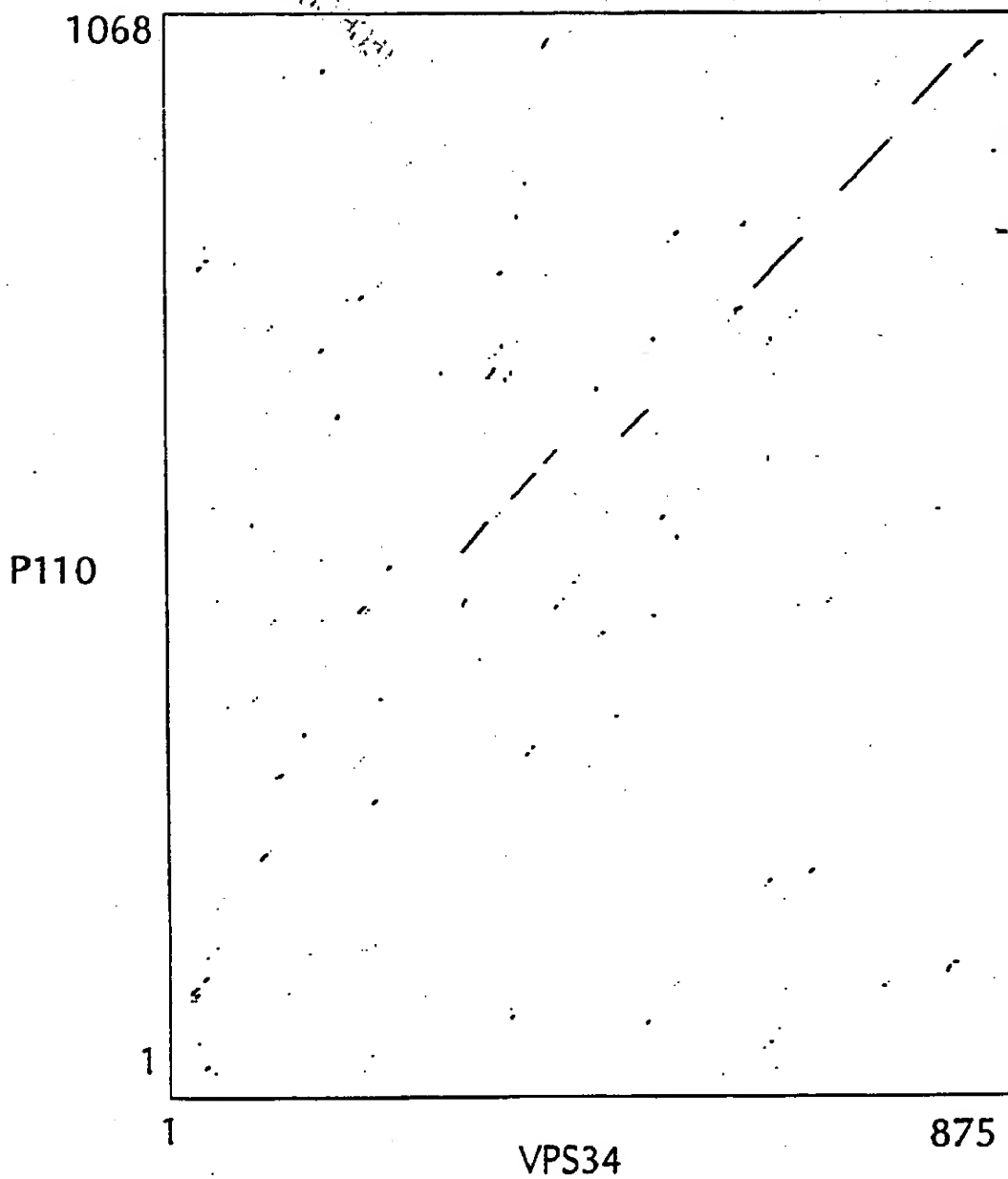




FIG. 10A





P110	VCEFD MVKDPEVQDFRRN ILNVCKEAVDLRDLNSPHSRAMYVYPPN	170
	.. :. : : . :: . :: . : :. :...	
VPS34	NITFCVSQDLDPV . LKVKIKSLEGHKPLLKPSQKITLNP ELM LIGSN	49
171	VESSPEL..PKHIY NKLDKGQIIVVIWVIVSPNNDKQKYTLKINHDCVPE	218
	. : . : : : . : : : :. : : : : : :	
50	VFPSSDLIVSLQVFDKERNRNLTLPYITPYIPFRNSRTWDYWL.....	92
219	QVIAEATRKKTRSM LLSSEQ LKLCVLEYQ GKYTLK VCGCDEYFLEKYPLS	268
	... : : : : : : : : : : .	
93TLP IRIKQLTFSS .HLRIILWEYNG.....	116
269	QYKYTRSCIMLGRMPNIMLMAKESLYSOLPMDCFIMPSYSRRISTATPYM	318
	... : :	
117SKQIPFF	123
319	NGETSTKSLWVINSALRIKILCATYVNVNIRDIDKIYVRTGIYHGGEPLC	368
	. : : : : : : : : : . : : . . : .	
124	NLETSI..FNLKDCTLK.....RGFESLKFYDVIDHCEVVT	158
369	DNVNTQ RVPCSNPRWNEWLN YDIYIPDL PRAARLC .LSICSVKGRKGAKE	417
	: . .. : : : : : : : : : : :	
159	DNKD.....QENLN .KYFQGEFTRL PWLDEITISKLRKQENRT	196

FIG. 10C



657 ALTNQRIGHFFFWHLKSEMHNKTVSQRFGILLLESY.CRACGMYLKHLNRQ 705
|||.||:| ||:|.|||| :|. :. :|.||: :| . . || |
488 ALVNPRLGSEFFYWYLKSESEDKPY...LDQILSSFWRLDKKSRNILDQ 534
706 VEAMEKLINLTDILKQEKKDETQKVQMKF.LVEQMRRPDMDALQGF LSP 754
| :. :| : :. :|. |.....|: :. :|:| . || : :. :|
535 VRLINVLRECCETIKRLKDTAKKMELLVHLLKETKVRP..LVKVRPIALP 582
755 LNPALQGLNLRLEECRIMSSAKRPLWLNWENPDIMSELLFONNEIIFKNG 804
|:|. :. :. |: :. :|. . ||: :. :. :. :| :. :|| |
583 LDPDVLICDVCPESTKVFKSSLSPLKITFKTT.....LNQPYHLMFKVG 626
*
805 DDLRQDMLTLQIIRIMENIWQNOGLDLRMLPYGCLSIGDCVGLIEVVRNS 854
||||| |.:|||.:|: :. :|. :. :||: || .|.|. | ||.:|
627 DDLRQDQVLVQIISLMNELLKNENVDLKLTPYKILATGPOEGATEFIPN. 675
*
855 HTIMQIQCK.GGLKQALQFNSHTLHQWLKDKNKGEIYDAIDLETRSCAG 903
.:| :| :| :| :. :. :. :. :. :. :. :. :| :.:|||
676 DTLASILSKYHGILGYLKL.....HYPDENATLGVOGWVLDNEVKSCAG 719
* * *
904 YCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVP 953
||| |.:|||:|||| |.:|..||: :|| |||.:|: :. :|. | |
720 YCVITYILGVGDRHLDNLLVTPDGHFFHADEFGYILGQDPKPF.....P 762
954 FVLTQDFLIVISKGAQECTKTREFERFQEMCYKAYLAIRQHANLFINLS 1003
:. . |.: |.:|. :. :. :. :. :. :. :. :. :| :.:|. :.:|||. :
763 PIMKLPPQIIEAFGGAESS...NYDKERSYCFVAYSILRRNAGLIILNLE 809
1004 MMLGSGMPE..LQSFDDIAYIRKTLALDKTEQEALEYFMKQNDAAHGGW 1051
:| .|. :| :. :. :| :|. :. :|. :. :| :| .|. :||. :. :
810 IMKTSNIPDIRIDPNGAILVRERENLNMSEEDATVHFQNLINDSVNALL 859
1052 TTKMDWIFHTIKQH 1065
.. :| :|:|. |.
860 PIVIDH.LHNLAQY 872



FIG. 11A

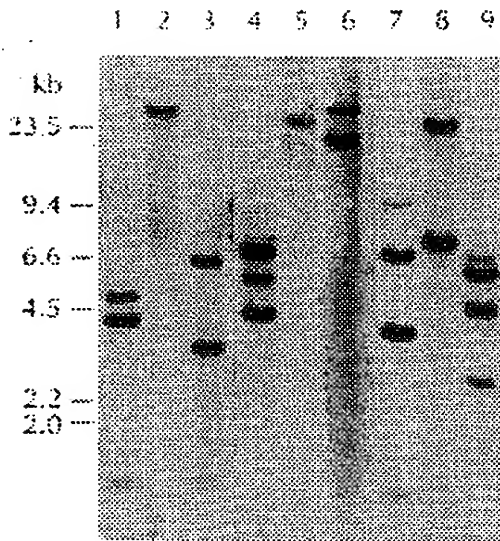


FIG. 11B

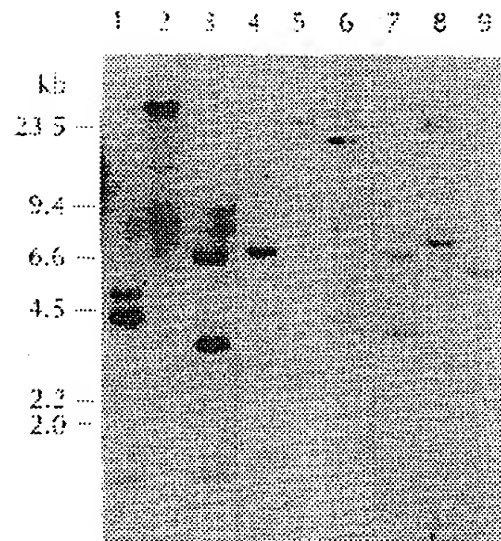
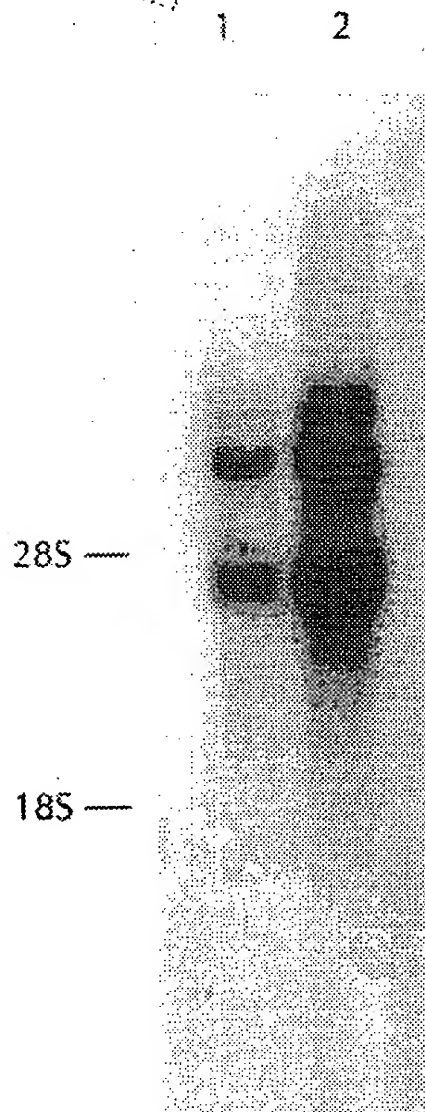




FIG. 12A



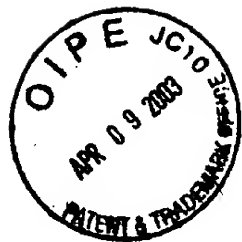


FIG. 12B

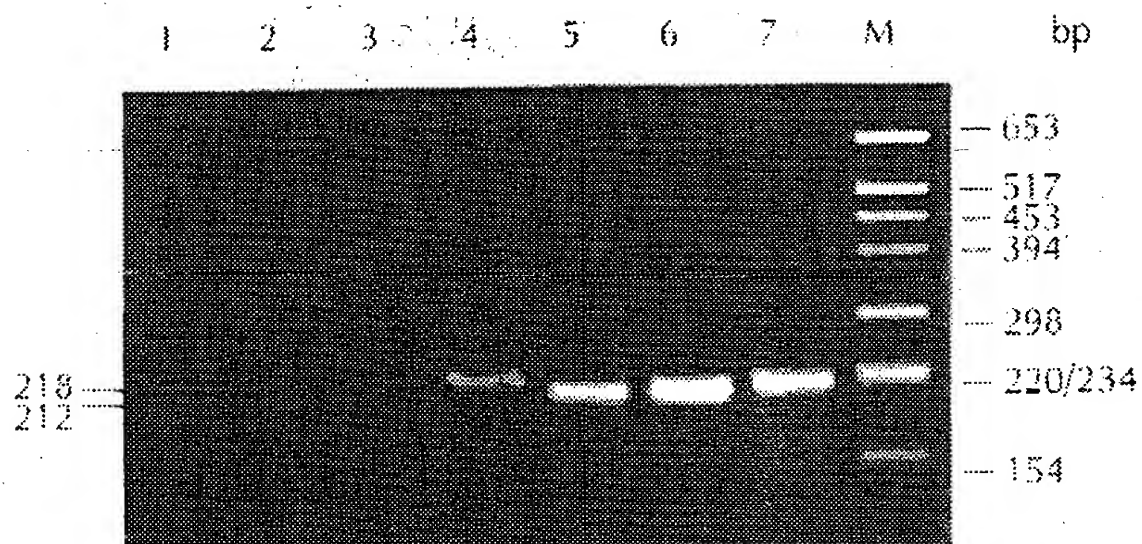


FIG. 12C

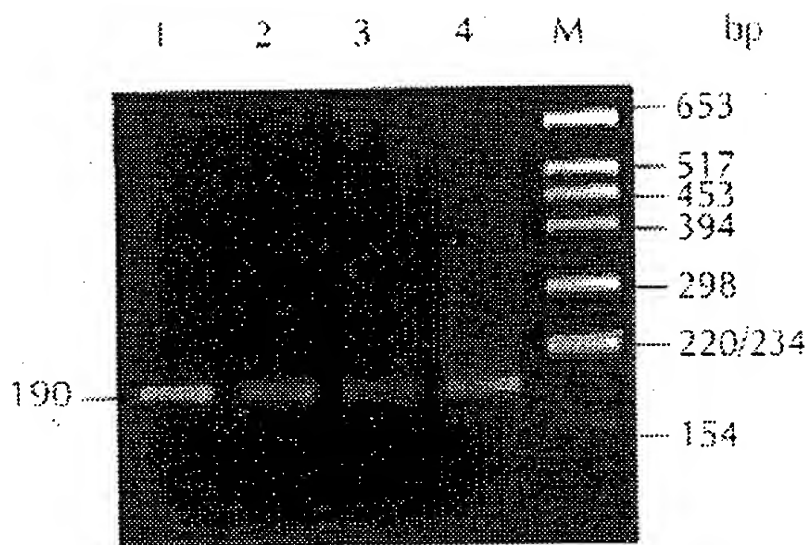




FIG. 13A

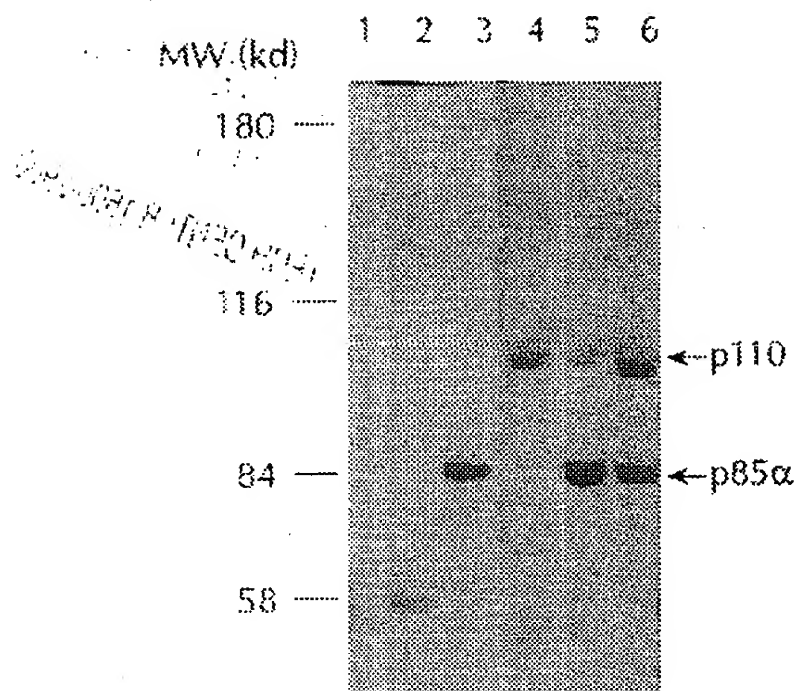


FIG. 13B

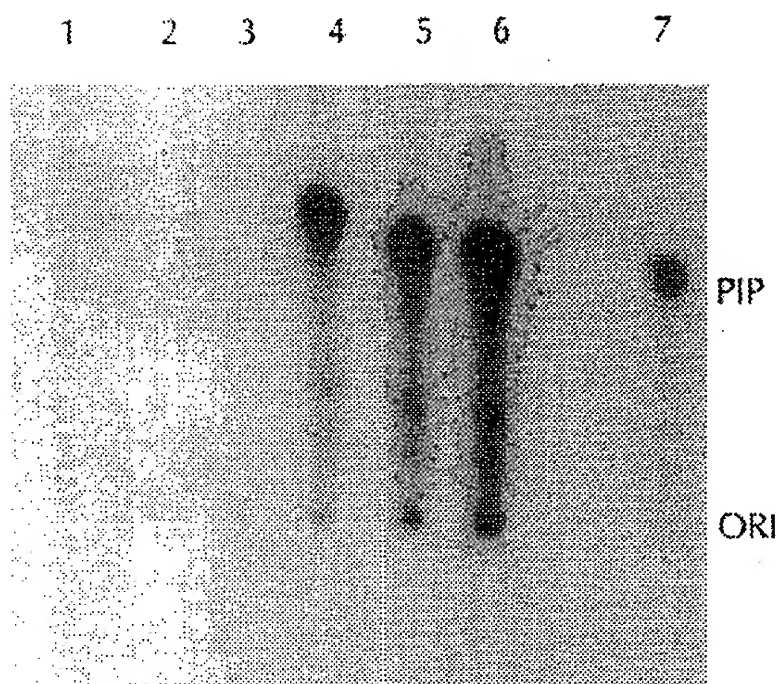




FIG. 14A

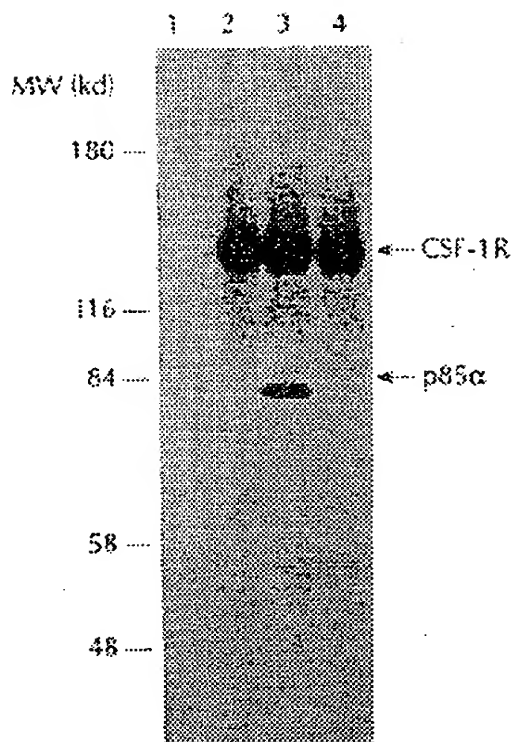


FIG. 14B

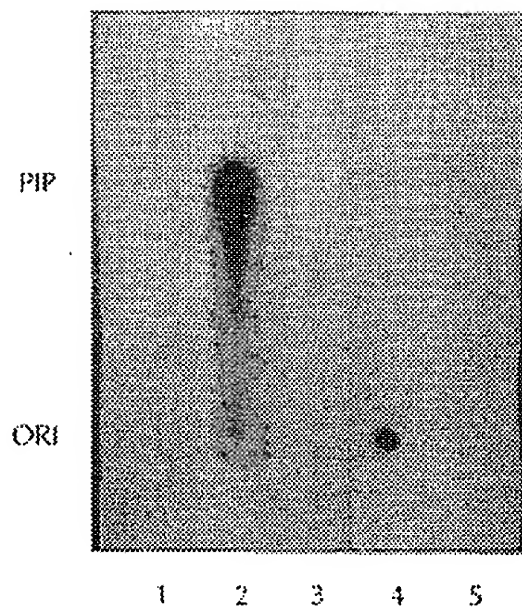


FIG. 15A

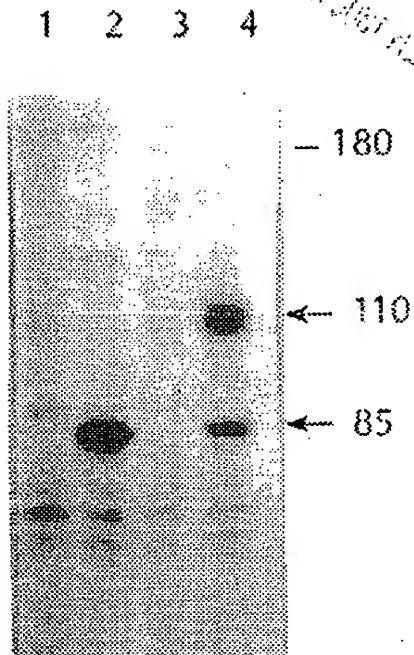


FIG. 15B

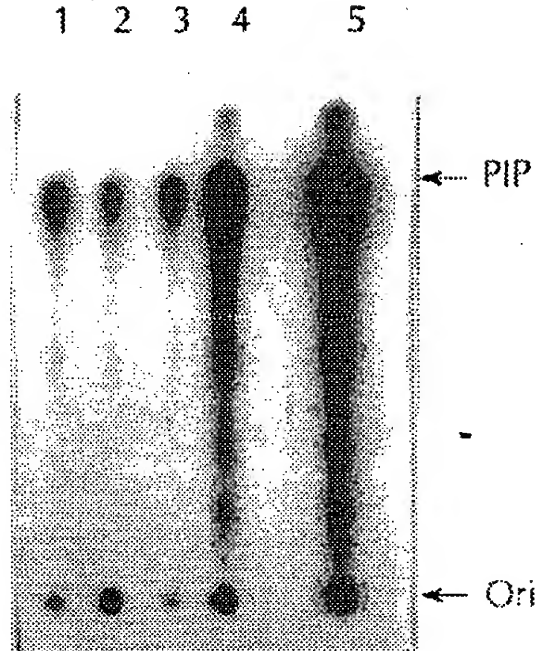


FIG. 15C

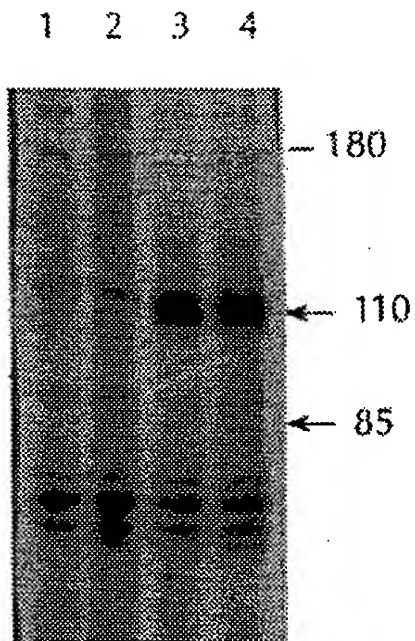


FIG. 15D

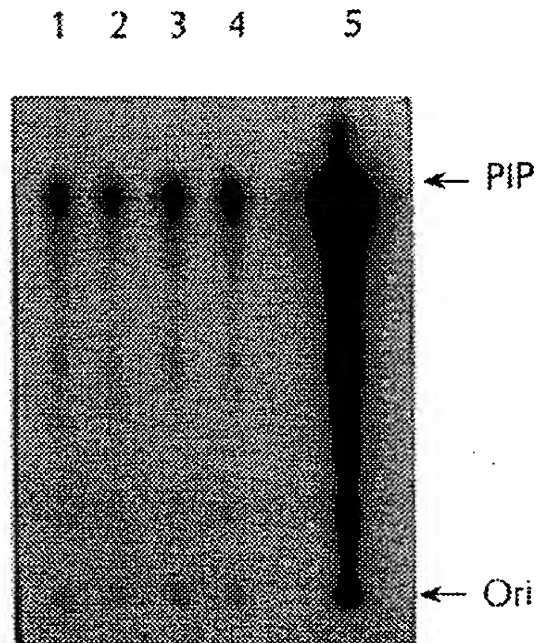




FIG. 16A

1 ATGCCTCCAAGACCATCATCAGGTGAACCTGTGGGGCATCCACTTGATG 48
-----+-----+-----+-----+-----+-----
TACGGAGGTTCTGGTAGTAGTCCACTTGACACACCCCGTAGGTGAACCTAC
M P P R P S S G E L W G I H L M
49 CCCCCAAGAATCCTAGTGGAAATGTTTACTACCAAAATGGAATGATAGTG 96
-+-----+-----+-----+-----+-----+-----
GGGGGTTCTTAGGATCACCTTACAAATGATGGTTTACCTTACTATCAC
P P R I L V E C L L P N G M I V
97 ACTTTAGAAATGCCCTCCGTGAGGCTACATTAGTAACTATAAAGCATGAA 144
---+-----+-----+-----+-----+-----+-----
TGAAATCTTACGGAGGCACCTCCGATGTAATCATTTGATATTTTCGTACTT
T L E C L R E A T L V T I K H E
145 CTATTTAAGAAGCAAGAAATACCCCTCTCCATCAACTTCTTCAAGAT 192
-----+-----+-----+-----+-----+-----+-----
GATAAATTCTTCGTTCTTTATGGGAGAGGTAGTTGAAGAAGTTCTA
L F K E A R K Y P L H Q L L Q D

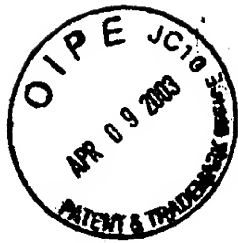


FIG. 16B

193 GAATCTTCTTACATTTTCGTAAAGTGTTACCCAAAGAACGAGAAAGGGAA
-----+-----+-----+-----+-----+-----+
CTTAGAAGAAATGTAAAGCATTCACAATGGGTTCTTCGTCTTTCCCTT
E S Y I F V S V T Q E A E R E 240

241 GAATTTTGTGATGAAACAAGACGACTTTGTGATCTTCGGCTTTTCAA
-----+-----+-----+-----+-----+-----+
CTTAAAAACTACTTTGTCTCTGCTGAAACACTAGAACCCGAAAGTT
E F F D E T R R L C D L R L F Q 288

289 CCATTTTAAAGTAATTGAACCAGTAGGCAACCGTGAAAGAAAGATC
-----+-----+-----+-----+-----+-----+
GGTAAAAATTTTCATTAACCTTGGTCATCCGTTGGCACTTCTTTCTAG
P F L K V I E P V G N R E E K I 336

337 CTCAATCGAGAAAATTGGTTTGTCTATCGGCATGCCAGTGTGCGAATTT
-----+-----+-----+-----+-----+-----+
GAGTTAGCTCTTTAAACCAAAACGATAGCCGTACGGTCACACGCTTAAA
L N R E I G F A I G M P V C E F 384

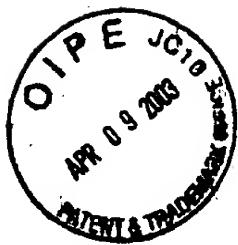
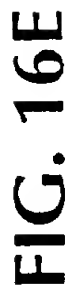


FIG. 16C

[illegible]

[illegible]



769	TGTGATGAATACTTCCTAGAAAAAATATCCTCTGAGTCAGTATAAGTAT -+-----++-----+-----+-----+-----+ ACACTACTTATGAAGGATCTTTTATAGGAGACTCAGTCATATTCATA C D E Y F L E K Y P L S Q Y K Y	816
817	ATAAGAAGCTGTATAATGCTTGGGAGGATGCCCAATTIGAAGATGATG ---+-----+-----+-----+-----+-----+ TATTTCTCGACATATTACGAACCCCTCCTACGGGTTAAACTTCTACTAC I R S C I M L G R M P N L K M M	864
865	GCTAAAGAAAGCCCTTTATTCTCAACTGCCAATGGACTGTTTTACAATG ---+-----+-----+-----+-----+-----+ CGATTTCTTTCGGAAATAAGAGTTGACGGTTACCTGCACAAAATGTTAC A K E S L Y S Q L P M D C F T M	912
913	CCATCTTATTCCAGACGCATTTCCACAGCTACACCATATATGAATGGA ---+-----+-----+-----+-----+-----+ GGTAGAAATAAGGTCTGCGTAAAGGTGTCGATGTGGTATATACTTACCT P S Y S R R I S T A T P Y M N G	960



FIG. 16F

961	GAAACATCTACAAAATCCCTTTGGGTTATATAATAGAGCACTCAGAATA -----+-----+-----+-----+-----+----- CTTTGTAGATGTTTAGGAAACCCAATATTATCTCGTGAGTCTTAT E T S T K S L W V I N R A L R I	1008
1009	AAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGACATTGAC -+-----+-----+-----+-----+-----+----- TTTAAAGAAACACGTTGGATGCACCTTAGATTATATAAGCTCTGTAACTG K I L C A T Y V N L N I R D I D	1056
1057	AAGATTTATGTTCGAACAGGTATCTACCATGGAGGAGAACCCCTTATGT -+-----+-----+-----+-----+-----+----- TTCTAAATACAAGCTTGTCCATAGATGGTACCTCCTCTTGGGAATACA K I Y V R T G I Y H G G E P L C	1104
1105	GACAAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGAAT -+-----+-----+-----+-----+-----+----- CTGTTACACTTGTGAGTTTCTCATGGAACAAGGTTAGGTTCCACCTTA D N V N T Q R V P C S N P R W N	1152



FIG. 16G

1153 GAATGGCTGAATTATGATATATACATTCCCTGATCTTCCTCGTGTGCTGCT
-----+-----+-----+-----+-----+-----+
CTTACCGACTTAATACTATATATGTAAGGACTAGAAAGGACGACGACGA
E W L N Y D I Y I P D L P R A A 1200

1201 CGACTTTGCCCTTCCATTGTGCTCTGTAAAGGCCGAAAGGGTGCTAAA
-----+-----+-----+-----+-----+-----+
GCTGAAACGGAAAGGTAAACGAGACAATTTCCGGCTTTCCACGATTT
R L C L S I C S V K G R K G A K 1248

1249 GAGGAACACTGTCCATTGGCATGGGGAATAATAAACTTGTGTGATTAC
-+-----+-----+-----+-----+-----+-----+
CTCCTTGTGACAGGTAACCGTACCCCTTTATATATTGAACAACTAATG
E E H C P L A W G N I N L F D Y 1296

1297 ACAGACACTCTAGTATCTGGAATAATGGCTTTGAATCTTTGGCCAGTA
---+-----+-----+-----+-----+-----+-----+
TGTCTGTGAGATCATAGACCTTTTACCGAACTTAGAAACCGGTCAT
T D T L V S G K M A L N L W P V 1344



FIG. 16H

1345 CCTCATGGATTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCA 1392
-----+-----+-----+-----+-----+-----+-----+-----+-----+
GGAGTACCTAATCTTCTAAACGACTTGGGATAACCAACAATGACCTAGT
P H G L E D L L N P I G V T G S

1393 AATCCAAATAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTC 1440
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TTAGGTTTATTCTTTGAGGTACGAATCTCAACCTCAAACCTGACCAAG
N P N K E T P C L E L E F D W F

1441 AGCAGTGTGGTAAAGTTCCCAGATATGTCAGTGATTGAAGAGCATGCC 1488
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TCGTCACACCATTTCAAGGGTCTATACAGTCACCTAACTTCTCGTACGG
S S V V K F P D M S V I E E H A

1489 AATTGGTCTGTATCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGA 1536
-----+-----+-----+-----+-----+-----+-----+-----+-----+
TTAACCCAGACATAGGGCTCTTCGTCCTTAATCGATAAGGTGCGTCCT
N W S V S R E A G F S Y S H A G

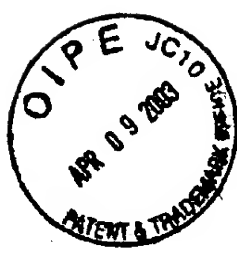


FIG. 161

1537	CTGAGTAACAGACTAGCTAGAGACAAATGAATTAAGGGAATAATGACAAA -----+-----+-----+-----+-----+----- GACTCATTTGCTGATCGATCTCTGTACTTAATTCCTTTTACTGTTT L S N R L A R D N E L R E N D K	1584
1585	GAACAGCTCAAAGCAATTCTACACGAGATCCTCTCTCTGAAATCACT -----+-----+-----+-----+-----+----- CTTGTCGAGTTTCGTTAAAGATGTGCTCTAGGAGAGAGACTTTAGTGA E Q L K A I S T R D P L S E I T	1632
1633	GAGCAGGAGAAAGATTTTCTATGGAGTCACAGACACTATTGTGTAAC -----+-----+-----+-----+-----+----- CTCGTCCCTCTTTCTAAAGATAACCTCAGTGTCTGTGATAACACATTGA E Q E K D F L W S H R H Y C V T	1680
1681	ATCCCCGAAATTCTACCCCAAATTGCTTCTGTCTGTAAATGGAATTCT -----+-----+-----+-----+-----+----- TAGGGGCTTTAAGATGGGTTTAAACGAAGACAGACAATTTACCTTAAGA I P E I L P K L L L L S V K W N S	1728



FIG. 16J

1729 AGAGATGAAGTAGCCAGATGTATTGCTTGGTAAAGATTGGCCTCCA 1776
-+-----+-----+-----+-----+-----+-----+-----+-----+
TCTCTACTTCATCGGGTCTACATAACGAACCATTTTCTAACCGGAGGT
R D E V A Q M Y C L V K D W P P

1777 ATCAAACCTGAACAGGCTATGGAACCTTCTGGACTGTAATTACCCAGAT 1824
-+-----+-----+-----+-----+-----+-----+-----+-----+
TAGTTTGGAAGCTTGTCCGATACCTTGAAGACCTGACATTAATGGGTCTA
I K P E Q A M E L L D C N Y P D

1825 CCTATGGTTCGAGGTTTGTGCTGTTCCGGTCTTGGAAAAATATTTAACA 1872
-----+-----+-----+-----+-----+-----+-----+-----+
GGATACCAAGCTCCAAAACGACAAGCCACGAAACCTTTTATATAAATTGT
P M V R G F A V R C L E K Y L T

1873 GATGACAAACTTCTCAGTATTTAATTTCAGCTAGTACAGGTCCTAAAA 1920
-----+-----+-----+-----+-----+-----+-----+-----+
CTACTGTTTGAAAGAGTCATAAATTAAAGTCGATCATGTCCAGGATTTT
D D K L S Q Y L L I Q L V Q V L K



FIG. 16K

1921 TATGAACAATATTGGATAACTTGCTTGTGAGATTTTACTGAAGAAA
-----+-----+-----+-----+-----
ATACTTGTATAAACCTATTGAACGAACACTCTAAAAATGACTTCTTT
Y E Q Y L D N L L V R F L L K K

1968

1969 GCATTGACTAATCAAAGGATTGGCAGCTTTTCTTTTGGCATTTAAAA
-----+-----+-----+-----+-----
CGTAACTGATTAGTTTCCTAACCCGTGAAAAAGAAAAACCGTAAATTTT
A L T N Q R I G H F F F W H L K

2016

2017 TCTGAGATGCACAATAAAACAGTTAGCCAGAGGTTTGGCCTGCTTTTG
-----+-----+-----+-----+-----
AGACTCTACGTGTTATTTTGTCAATCGGTCTCCAAACCGGACGAAAC
S E M H N K T V S Q R F G L L L

2064

2065 GAGTCCTATTGTCGTGCATGTGGGATGTATTTGAAGCACCTGAATAGG
-----+-----+-----+-----+-----
CTCAGGATAACAGCACGTACACCCCTACATAAACTTCGTGGACTTATCC
E S Y C R A C G M Y L K ' H L N R

2112



FIG. 16L

2113 CAAGTCGAGGCAATGGAAGCTCATTAACCTTAACCTGACATTTCTCAAA
-----+-----+-----+-----+-----+-----+
GTTCAGCTCCGTTACCTTTTCGAGTAATTGAATTGACTGTAAGAGTTT
Q V E A M E K L I N L T D I L K

2160

2161 CAGGAGAGGAAGGATGAACACAAAGGTACAGATGAAGTTTTAGTT
-----+-----+-----+-----+-----+-----+
GTCCTCTCCTTCCCTACTTTGTGTTTTCCATGTCTACTTCAAAAATCAA
Q E R K D E T Q K V Q M K F L V

2208

2209 GAGCAAATGAGCGCACCAGATTTTCATGGATGCCCTACAGGGCTTGCTG
-+-----+-----+-----+-----+-----+-----+
CTCGTTTACTCCGCTGGTCTAAAGTACCTACGGGATGTCCCGAAGGAC
E Q M R R P D F M D A L Q G L L

2256

2257 TCTCCTCTAAACCCCTGCTCATCAACTAGGAAACCTCAGGCTTAAAGAG
---+-----+-----+-----+-----+-----+-----+
AGAGGAGATTGGGACGAGTAGTTGATCCCTTTGGAGTCCGAATTCTC
S P L N P A H Q L G N L 'R L K E

2304



2497 ATGTTACCTTATGGTTGTTCTGTCAATCGGTGACTGTGTGGACTTATT
-+-----+-----+-----+-----+-----+-----+
TACAATGGAATACCAACAGACAGTTAGCCACTGACACACCCCTGAATAA
M L P Y G C L S I G D C V G L I
2592 GAGTGGTGCGAAATTCTCACACTATTATGCAAATTCAGTGCAAAGGC
-+-----+-----+-----+-----+-----+-----+
CTCCACCACGCTTTAAGAGTGTGATAATAACGTTTAAGTCACGTTTCCG
E V V R N S H T I M Q I Q C K G
2640 GGCTTGAAAGTGCACTGCAGTTCAACAGCCACACACTACATCAGTGG
-+-----+-----+-----+-----+-----+-----+
CCGAACCTTCCACGTGACGTCAAGTTGTCGGTGTGTGATGTAGTCACC
G L K G A L Q F N S H T L H Q W
2688 CTCAAAGACAAGAACAAAGGAGAAATATATGATGCAGCCATTGACCTG
-+-----+-----+-----+-----+-----+-----+
GAGTTTCTGTTCTTGTTCCTCTTTATATACTACTACGTCGGTAACTGGAC
L K D K N K G E I Y D A A I D L



FIG. 160

2689 TTTACCGTTCAATGCTGGATACTGTGTAGCTACCTTCATTTTGGGA
-+-----+-----+-----+-----+-----+-----+
AAATGTGCAAGTACACGACCTATGACACATCGATGGAAGTAAACCCCT
F T R S C A G Y C V A T F I L G 2736

2737 ATTGGAGATCGTCACAATAGTAACATCATGGTGAAAGACGATGGACAA
-+-----+-----+-----+-----+-----+-----+
TAACCTCTAGCAGTGTATCATTTGTAGTACCACCTTTCTGCTACCTGTT
I G D R H N S N I M V K D D G Q 2784

2785 CTGTTTCATATAGATTTTGGACACACTTTTGGATCACAAGAAAGAAAAA
-+-----+-----+-----+-----+-----+-----+
GACAAAGTATATCTAAACCTGTGAAACCTAGTGTCTTCTTTT
L F H I D F G H F L D H K K K K 2832

2833 TTTGGTTATAACGAGAACGTGTGCCATTTGTTTTCACACAGGATTC
-+-----+-----+-----+-----+-----+-----+
AAACCAATATTGCTCTTGCACACGGTAAACAAACCTGTGTCCTAAAG
F G Y K R E R V P F V L T Q D F 2880



FIG. 16P

2881 TTAATAGTGATTAGTAAAGGAGCCCAAGAAATGCACAAAGACAAGAGAA
-----+-----+-----+-----+-----+-----
AATTATCACTAATCATTTCCCTCGGGTTCTTACGTGTTTCTGTCTCTT
L I V I S K G A Q E C T K T R E
2928

2929 TTGAGAGGTTTCAGGAGATGTGTACAAGGCTTATCTAGCTATTCTGA
-----+-----+-----+-----+-----+-----
AAACTCTCCAAGTCCCTCTACACAAATGTTCCGAATAGATCGATAAGCT
F E R F Q E M C Y K A Y L A I R
2976

2977 CAGCATGCCAAATCTCTCATAAAATCTTTTCTCAATGATGCTTGGCTCT
-----+-----+-----+-----+-----+-----
GTCGTACGGTTAGAGAAAGTATTTAGAAAGAGTTACTACGAACCGAGA
Q H A N L F I N L F S M M L G S
3024

3025 GGAATGCCAGAACTACAATCTTTTGATGACATTGCATACATTCGAAAG
-----+-----+-----+-----+-----+-----
CCTTACGGTCTTGATGTTAGAAAACACTACTGTAACGTATGTAAAGCTTTC
G M P E L Q S F D D I A Y I R K
3072



FIG. 16Q

3073	ACCCTAGCCTTAGATAAACTGAGCAAGAGGCTTTGGAGTATTTCATG -----+-----+-----+-----+-----+-----+ TGGGATCGGAATCTATTTTGACTCGTTCTCCGAAACCTCATAAAGTAC T L A L D K T E Q E A L E Y F M	3120
3121	AAACAAATGAATGATGCACATCATGGTGGCTGGACAACAAAATGGAT -----+-----+-----+-----+-----+-----+ TTTGTTTACTTACTACGTGTAGTACCACCGACCTGTTGTTTACCTA K Q M N D A H H G G W T T K M D	3168
3169	TGGATCTTCCACACAATTAAACAGCATGCATTGAACTGAAAGATAACT --+-----+-----+-----+-----+-----+-----+ ACCTAGAAGGTGTGTTAATTGTGCGTACGTAACCTTGACTTTCTATTGA W I F H T I K Q H A L N *	3216
3217	GAGAAAATGAAAGCTCACTCTGGATTCCACACTGCACCTGTTAATAACT --+-----+-----+-----+-----+-----+-----+ CTCTTTTACTTTCGAGTGAGACCCTAAGGTGTGACGTGACAATTATTGA	3264



3265 CTCAGCAGGCAAGACCGATTGCATAGGAATTGCACAAATCCATGAACA
 ---+-----+-----+-----+-----+-----+-----+
 3312 GAGTCGTCGGTTCTGGCTAACGTATCCTTAACGTGTAGGTACTTGT



FIG. 17A

hum110 1 ATGCCCTCCAAGACCATCATCAGGTGAACCTGTGGGGCATCCACTTGATGCC 50
|||||
bov110 1 ATGCCCTCCAAGACCATCATCAGGTGAACCTGTGGGGCATCCACTTGATGCC 50
|||||
51 CCCAAGAATCCTAGTGGAATGTTACTACCAAAATGGAATGATAGTGACTT 100
|||||
51 CCCAAGAATCCTAGTAGAATGTTTACTACCAAAATGGGATGATAGTGACTT 100
|||||
101 TAGAATGCCCTCCGTGAGGCTACATTAGTAACCTATAAAGCATGAACCTATTT 150
|||||
101 TAGAATGCCCTCCGTGAGGCTACGTTAATAACGATAAAGCATGAACCTATTT 150
|||||
151 AAAGAAGCAAGAAATAACCCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200
|||||
151 AAAGAAGCAAGAAATAACCCCTCTCCATCAACTTCTTCAAGATGAATCTTC 200



FIG. 17C

451 GTGGATCTTAGGGATCTTAATTCACCTCATAGTAGCAATGTATGTCTA 500
|||||
451 GTGGATCTTAGGGATCTTAATTCACCTCATAGTAGCAATGTATGTTTA 500
|||||
501 TCCGCCACATGTAGAAATCTTACCAGAGCTGCCAAAGCACATATAATA 550
|||||
501 TCCTCCAAATGTAGAAATCTTACCAGAACTGCCAAAGCACATATAATA 550
|||||
551 AATTGGATAGAGGCCAAATAATAGTGGTGATTGGGTAATAGTTCTCCA 600
|||||
551 AATTGGATAAAGGGCAAATAATAGTGGTGATTGGGTAATAGTTCTCCA 600
|||||
601 AATAATGACAAGCAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650
|||||
601 AATAATGACAACACAGAAGTATACTCTGAAAATCAACCATGACTGTGTGCC 650
|||||
651 AGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTAGAAGTATGTTGC 700
|||||
651 AGAACAAAGTAATTGCTGAAGCAATCAGGAAAAAACTCGAAGTATGTTGC 700



FIG. 17D

701 TATCATCTGAACAATTAAAACTCTGTGTTTGAATATCAGGCAAGTAC 750
|||||
701 TATCATCTGAACAACAATAAACTCTGTGTTTGAATATCAGGCAAGTAT 750
|||||
751 ATTTTAAAGTGTGGATGTGATGAATACTTCTAGAAAATATCCTCT 800
|||||
751 ATTTTAAAGTGTGGATGTGATGAATACTTCTAGAAAATATCCTCT 800
|||||
801 GAGTCAGTATAAGTATAAAGAAGCTGTATATGCTTGGAGGATGCCCA 850
|||||
801 GAGTCAGTATAAGTATAAAGAAGCTGTATATGCTTGGAGGATGCCCA 850
|||||
851 ATTTGAAGATGATGGCTAAAGAAAGCCTTTATTCTCAACTGCCAATGGAC 900
|||||
851 ATTTGATGCTGATGGCTAAAGAAAGCCTCTATTCTCAACTGCCAATGGAC 900
|||||
901 TGTTTTACAATGCCATCTTATTCCAGACGCATTTCCACAGCTACACCATA 950
|||||
901 TGTTTTACAATGCCATCATATATCCAGACGCATCTCCACAGCTACGCCATA 950



FIG. 17E

951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGAGCAC 1000
|||||
951 TATGAATGGAGAAACATCTACAAAATCCCTTTGGGTTATAAATAGTGCAC 1000
|||||

1001 TCAGAAATAAAAATTCTTTGTGCAACCTACGTGAATCTAAATATTCGAGAC 1050
|||||
1001 TCAGAAATAAAAATTCTTTGTGCAACCTATGTGAATGTAAATATTCGAGAC 1050
|||||

1051 ATTGACAAAGATTATGTTTCGAACAGGTATCTACCATGGAGGAGAACCCCTT 1100
|||||
1051 ATTGACAAAGATTATGTTTCGAACAGGTATCTACCATGGAGGAGAACCCCTT 1100
|||||

1101 ATGTGACAAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150
|||||
1101 ATGTGATAATGTGAACACTCAAAGAGTACCTTGTTCCAATCCCAGGTGGA 1150
|||||

1151 ATGAATGGCTGAATTATGATATATACATTCCCTGATCTTCCTCGTGCTGCT 1200
|||||
1151 ATGAATGGCTGAATTACGATATATACATTCCCTGATCTTCCTCGTGCTGCT 1200
|||||

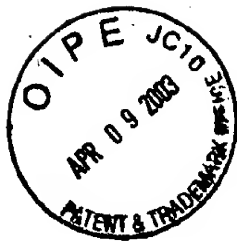


FIG. 17F

1201 CGACTTTGCCCTTTCCATTGCTCTGTAAAGGCCGAAAGGTGCTAAAGA 1250
|||||
1201 CGACTTTGCCCTTTCCATTGCTCTGTAAAGGCCGAAAGGTGCTAAAGA 1250
1251 GGAACACTGTCCATTGGCATGGGGAATAATAAACTTGTGATTACACAG 1300
|||||
1251 GGAACACTGTCCATTGGCCCTGGGGAATAATAAACTTGTGATTACACAG 1300
1301 AACTCTAGTATCTGGAAAATGGCTTTGAATCTTTGGCCAGTACCTCAT 1350
|||||
1301 AACTCTAGTATCTGGAAAATGGCTTTGAATCTTTGGCCAGTACCTCAT 1350
1351 GGATTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCAAATCCAAA 1400
|||
1351 GGACTAGAAGATTGCTGAACCCCTATTGGTGTACTGGATCAAATCCAAA 1400
1401 TAAAGAACTCCATGCTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450
|||||
1401 TAAAGAACTCCATGTTTAGAGTTGGAGTTTGACTGGTTCAGCAGTGTGG 1450



1451	TAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1500
1451	TAAAGTTCCAGATATGTCAGTGATTGAAGAGCATGCCAATTGGTCTGTA	1500
1501	TCCCGAGAAGCAGGATTTAGCTATTCCCACGCAGGACTGAGTAACAGACT	1550
1501	TCCCGTGAAGCAGGATTTAGTTATTCCCATGCAGGACTGAGTAACAGACT	1550
1551	AGCTAGAGACAAATGAATTAAAGGGAATAATGACAAAGAACAGCTCAAAGCAA	1600
1551	AGCTAGAGACAAATGAATTAAAGAGAAATGATAAGAACAGCTCCGAGCAA	1600
1601	TTTCTACACGAGATCCTCTCTCTGAAATCACTGAGCAGGAGAAAGATTTT	1650
1601	TTTGTACACGAGATCCTCTATCTGAAATCACTGAGCAAGAGAAAGATTTT	1650
1651	CTATGGAGTCACAGACACTATTGTGTAACCTATCCCCGAAATTCTACCCAA	1700
1651	CTGTGAGCCACAGACACTATTGTGTAACCTATCCCCGAAATTCTACCCAA	1700

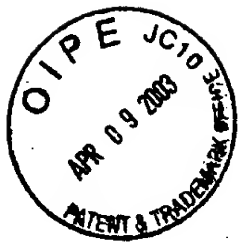


FIG. 17H

1701 ATTGCTTCTGCTGTTAAATGGAAATCTAGAGATGAAGTAGCCAGATGT 1750
|||||
1701 ATTGCTTCTGCTGTTAAATGGAACTCTAGAGATGAAGTAGCTCAGATGT 1750
|||||
1751 ATTGCTTGGTAAAGATTGGCCCTCCAATCAAACCTGAACAGGCTATGGAA 1800
|||||
1751 ACTGCTTGGTAAAGATTGGCCCTCCAATCAAGCCTGAACAGGCTATGGAG 1800
|||||
1801 CTTCTGGACTGTAATTACCCAGATCCTATGGTTCGAGGTTTGTGCTGTTCCG 1850
|||||
1801 CTTCTGGACTGCAATTACCCAGATCCTATGGTTCGAGGTTTGTGCTGTTCCG 1850
|||||
1851 GTGCTTGGAAAAATATTAAACAGATGACAAACTTCTCAGTATTTAATTC 1900
|||||
1851 GTGCTTAGAAAAATATTAAACAGATGACAAACTTCTCAGTACCCTAATTC 1900
|||||
1901 AGCTAGTACAGGTCCTAAATAATGAACAATATTGGATAACTTGCTTGTTG 1950
|||||
1901 AGCTAGTACAGGTACTAAAAATATGAACAGTATTGGATAACCTGCTTGTTG 1950



FIG. 17J

2201 TTTTAGTTGAGCAAAATGAGGCGACAGATTTCATGGATGCCCTACAGGGC 2250
|||||
2201 TTTTAGTTGAGCAAAATGCGGCGACAGATTTCATGGATGCTCTCCAGGGC 2250
|||||
2251 TTGCTGTCTCCTCTAAACCCCTGCTCATCACTAGGAAACCTCAGGCTTAA 2300
||
2251 TTTCTGTCTCCTCTAAACCCCTGCTCATCAGCTGGGAAATCTCAGGCTTGA 2300
|||||
2301 AGAGTGTGCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGG 2350
|||||
2301 AGAGTGTGCGAATTATGTCTTCTGCAAAAAGGCCACTGTGGTTGAATTGGG 2350
|||||
2351 AGAACCCAGACATCATGTCTCAGAGTTACTGTCTTCAGAAACAATGAGATCATC 2400
|||||
2351 AGAACCCAGACATCATGTCTCAGAAATTACTCTTTCAGAAACAATGAGATCATC 2400
|||||
2401 TTTAAAAATGGGGATGATTACGGCAAGATATGCTAACACTTCAAATTAT 2450
|||||
2401 TTTAAAAATGGGGATGATTACGGCAAGATATGCTAACCCCTTCAGATTAT 2450

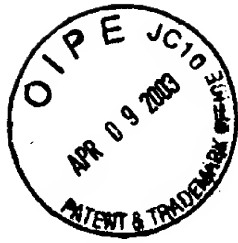


FIG. 17L

2701 TGTGCTGGATACTGTGTAGCTACCTTCATTTTGGGAATTGGAGATCGTCA 2750
|||||
2701 TGTGCTGGATAATTGTGTGCCACCTTCATTTTGGGAATTGGAGATCGTCA 2750
|||||
2751 CAATAGTAACATCATGGTGAAAGACGATGGACAACCTGTTTCATATAGATT 2800
|||||
2751 CAATAGTAATATCATGGTTAAAGATGATGGACAACCTGTTTCATATAGATT 2800
|||||
2801 TTGGACACTTTTGGATCACAAGAGAAAAATTGGTTATAAACGAGAA 2850
|||||
2801 TTGGACACTTTTGGATCACAAGAGAAAAATTGGTTATAAACGAGAG 2850
|||||
2851 CGTGTGCCATTGTGTTTGACACAGGATTCTTAATAGTGATTAGTAAAGG 2900
||
2851 CGCGTGCCGTTGTGTTTGACACACAAGATTCTTAATAGTGATTAGTAAAGG 2900
||
2901 AGCCCAAGAAATGCCACAAGACAAGAGAAATTGAGAGGTTTCAGGAGATGT 2950
|||||
2901 AGCCCAAGAAATGCCACAAGACAAGAGAAATTGAGAGGTTTCAGGAGATGT 2950

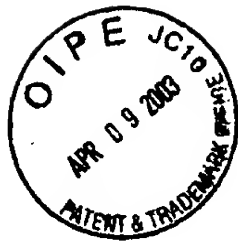


FIG. 17M

2951 GTTACAAGGCTTATCTAGCTATTGACAGCATGCCAATCTCTCATAAAT 3000
|||||
2951 GTTACAAGGCTTATCTAGCTATTGCGCAGCATGCCAATCTCTCATAAAT 3000
|||||
3001 CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTACAATCTTTTGA 3050
|||||
3001 CTTTTCTCAATGATGCTTGGCTCTGGAATGCCAGAACTGCAATCTTTTGA 3050
|||||
3051 TGACATTGCATACATTTCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAG 3100
|||
3051 TGATATTGCATACATTTCGAAAGACCCCTAGCCTTAGATAAACTGAGCAAG 3100
|||||
3101 AGGCTTTGGAGTATTTTCATGAAACAAATGAATGATGCACATCATGGTGGC 3150
|||||
3101 AGGCTTTGGAGTATTTTCATGAAACAAATGAATGATGCACACCATGGTGGC 3150
|||||
3151 TGGACAACAAAATGGATTGGATCTTCCACACAATTAACAGCATGCATT 3200
|||||
3151 TGGACAACAAAATGGATTGGATCTTCCACACAATTAAGCAGCATGCTTT 3200
|||||
3201 GAACTGAAAGATAAAGTGAAGAAATGAAAGCTCACTCTGGA
|||||
3201 GAACTGA.....



FIG. 18A

10	20	30	40	50	60
h	MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVTIKHELFKEARKYPLHQ				
b	MPPRPSSGELWGIHLMPPRILVECLLPNGMIVTLECLREATLVTIKHELFKEARKYPLHQ				
10	20	30	40	50	60
70	80	90	100	110	120
h	LLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFPQFLKVIKVPVGNREEKILNREIGFA				
b	LLQDESSYIFVSVTQEAEREEFFDETRRLCDLRLFPQFLKVIKVPVGNREEKILNREIGFA				
70	80	90	100	110	120
130	140	150	160	170	180
h	IGMPVCEFDVMDPEVQDFRRNILNVCKEAVDLRDLNSPHSRAMYVYPPHVESSPELPHK				
b	IGMPVCEFDVMDPEVQDFRRNILNVCKEAVDLRDLNSPHSRAMYVYPPHVESSPELPHK				
130	140	150	160	170	180

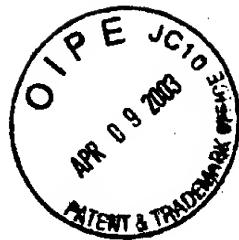


FIG. 18C

h YHGEPLCDNVNTQRVPCSNPRWNEWLNVDIYIPDLPRAAARLCLCSVKGRKGAKEEHC 420
||||| 380 390 400 410
b YHGEPLCDNVNTQRVPCSNPRWNEWLNVDIYIPDLPRAAARLCLCSVKGRKGAKEEHC 420
370 380 390 400 410

h PLAWGNINLFDYTDTLVSGKMAINLWVPVPHGLEDLLNPIGVTGSNPNKETPCLELEFDWF 480
||||| 440 450 460 470
b PLAWGNINLFDYTDTLVSGKMAINLWVPVPHGLEDLLNPIGVTGSNPNKETPCLELEFDWF 480
430 440 450 460 470

h SSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTRDPL 540
||||| 500 510 520 530
b SSVVKFPDMSVIEEHANWSVSREAGFSYSHAGLSNRLARDNELRENDKEQLKAISTRDPL 540
490 500 510 520 530

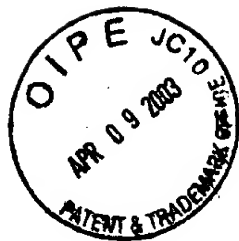


FIG. 18D

550 560 570 580 590 600
h SEITEQEKDFLWSHRHYCVTIPEILPKLLSVKWSRDEVAQMYCLVKDWPPIKPEQAME
|||||
b SEITEQEKDFLWSHRHYCVTIPEILPKLLSVKWSRDEVAQMYCLVKDWPPIKPEQAME
550 560 570 580 590 600

610 620 630 640 650 660
h LLDNCNYPDPMVRGFAVRCLEKYLTDKLSQYLIQLVQVLKYEQYLDNLLVRFLKKALTN
|||||
b LLDNCNYPDPMVRGFAVRCLEKYLTDKLSQYLIQLVQVLKYEQYLDNLLVRFLKKALTN
610 620 630 640 650 660

670 680 690 700 710 720
h QRIGHFFFHWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHLNRQVEAMEKLNLTDLK
|||||
b QRIGHFFFHWHLKSEMHNKTVSQRFGLLLESYCRACGMYLKHLNRQVEAMEKLNLTDLK
670 680 690 700 710 720



730	740	750	760	770	780
h	QERKDETQKVQMKFLVEQMRRPD	FMDALQGLSPLNPAHQ	GNLRLKECRIMSSAKRPLW		
	:				
b	QEKKDETQKVQMKFLVEQMRRPD	FMDALQGLSPLNPAHQ	GNLRLKECRIMSSAKRPLW		
	730	740	750	760	770

	850	860	870	880	890	900
h	IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKGEIYDAAIDLFTRS					
b	IGDCVGLIEVVRNSHTIMQIQCKGGLKGALQFNSHTLHQWLKDKNKGEIYDAAIDLFTRS					

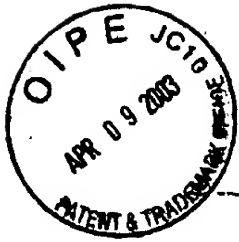


FIG. 18F

910	920	930	940	950	960
h	CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPVLTQDF				
b	CAGYCVATFILGIGDRHNSNIMVKDDGQLFHIDFGHFLDHKKKKFGYKRERVPVLTQDF				
910	920	930	940	950	960
970	980	990	1000	1010	1020
h	LIVISKGAQECTKTREFFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPELQSFDDIA				
b	LIVISKGAQECTKTREFFERFQEMCYKAYLAIRQHANLFINLFSMMLGSGMPELQSFDDIA				
970	980	990	1000	1010	1020
1030	1040	1050	1060	1070	1080
h	YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNXKITEKMKAHSG				
b	YIRKTLALDKTEQEALEYFMKQMNDAHHGGWTTKMDWIFHTIKQHALNX				
1030	1040	1050	1060		

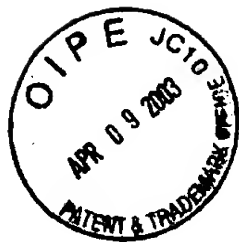


FIG. 19A

1	MPPRPSSGEL	WGIHLMPPRI	LVECLLPNGM	IVTLECLREA	TLVTIKHELF
51	KEARKYPLHQ	LLQDESSYIF	VSVTQEAERE	EEFDETRRLC	DLRLFQPFLLK
101	VIEPVGNREE	KILNREIGFA	IGMPVCEFDN	VKDPEVQDER	RNILNVCKEA
151	VDLRDLNSPH	SRAMYVYPPH	VESSPELPKH	IYNKLDRGQI	IVVIWVIVSP
201	NNDKQKYTLK	INHDCVPEQV	IAEAIRKKTR	SMLLSSEQLK	LCVLEYQGGY
251	ILKVCGCDEY	FLEKYPLSQY	KYIRSCIMLG	RMPNLKMMAK	ESLYSQLPMD
301	CFTMPYSRR	ISTATPYMNG	ETSTKSLWVI	NRALRIKILC	ATYVNLNIRD
351	IDKIYVRTGI	YHGGEPLCDN	VNTQVRPCSN	PRWNEWLNVD	IYIPDLPRAA
401	RLCLSICSVK	GRKGAKKEHC	PLAWGNINLF	DYTDTLVSGK	MAJNLWVPH
451	GLEDLNPIG	VTGSNPNKET	PCELELEFDWF	SSVVKFPDMS	VIEEHANWSV

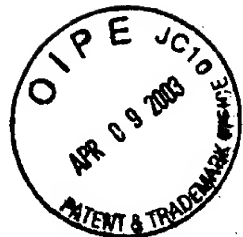


FIG. 19B

501 SREAGESYSH AGLSNRLARD NELRENDKEQ LKAISTRDPL SEITEQEKDF
551 LWSHRHYCVT IPEILPKLL SVKWSRDEV AQMYCLVKDW PPIKPEQAME
601 LLDCNYPDPM VRGFAVRCL KYLTDCLKSQ YLIQLVQVLK YEQYLDNLLV
651 RELKKALTN QRIGHEFFWH LKSEMHNKTV SQRFGLLES YCRACGMYLK
701 HLNROVEAME KLINLTDILK QERKDETQKV QMKFLVEQMR RPDFMDALQG
751 LLSPLNPAHQ LGNLRKPCR IMSSAKRPLW LNWENPDIMS ELLFQNNNEII
801 FKNGDDLQRD MLTLQIIRIM ENIWQNQGLD LRMLPYGCLS IGDCVGLIEV
851 VRNSHTIMQI QCKGGLKGAL QFNSHTLHQW LKDKNKGEIY DAAIDLFTRS
901 CAGYCVATFI LGIGDRHNSN IMVKDDGQLF HIDFGHFLDH KKKKFGYKRE
951 RVFVLTQDF LIVISKGAQE CTKTREFEF QEMCYKAYLA IRQHANLFIN
1001 LFSMMLGSGM PELQSFDDIA YIRKTLALDK TEQEALEYFM QOMNDAHGG
1051 WTTKMDWIFH TIKQHAIN*

FIG. 20

1 GGAGACGACTTGGACAGGATCAACTTATTCTTCAAAATCATTTCACTC
GlyAspLeuArgGlnAspGlnLeuIleLeuGlnIleIleSerLeu

49 ATGGACAAGCTGTACGGAAGAAATCTGGACTTGAAATTGACACCT
MetAspLysLeuLeuArgLysGluAsnLeuAspLeuLysLeuThrPro

97 TATAAGGTGTAGCCACCAGTACAAACATGGCTTCATGCAGTTATC
TyrLysValLeuAlaThrSerThrLysHisGlyPheMetGlnPheIle

145 CAGTCAGTtCCTGTGGCTGAaGTTCTTGATACAGAGGAAGCATTCAG
GlnSerValProValAlaGluValLeuAspThrGluGlySerIleGln

193 AACTTTTTTAGAAAATATGCACCAGTGAGAAATGGCCAAATGGGATT
AsnPhePheArgLysTyrAlaProSerGluAsnGlyProAsnGlyIle

241 AGTGCTGAGGTCA TGACACTtACGTTAAAAGCTGTGCTGGATATGC
SerAlaGluValMetAspThrTyrValLysSerCysAlaGlyTyrCys

289 GTGATCACCTATATACTTGGAGTTGGAGACAGGCACCTGGATAACCTT
ValIleThrTyrIleLeuGlyValGlyAspArgHisLeuAspAsnLeu

337 TTGCTAACCAAAACAGGCAAACTCTTCCACATCGATTTCGGCCAC
LeuLeuThrLysThrGlyLysLeuPheHisIleAspPheGlyHis



FIG. 21

1 GGGATGACTTACGGCAGGACATGCTAACGGTCAGATGATTCGCATC
GlyAspAspLeuArgGlnAspMetLeuThrLeuGlnMetIleArgIle

49 ATGAGCAAGATCTGGTCCAGAGGGGCTGGACATGCGCATGGTCATC
MetSerLysIleTrpValGlnGluGlyLeuAspMetArgMetValIle

97 TTCCGCTGCTTCTCCACCGCGCGGCGAGAGGGATGGTGGAGATGATC
PheArgCysPheSerThrGlyArgGlyArgGlyMetValGluMetIle

145 CCTAATGCTGAGACCCCTGCGTAAGATCCAGGTGGAGCATGGGTGACC
ProAsnAlaGluThrLeuArgLysIleGlnValGluHisGlyValThr

193 GGCTCGTTCAAGGACCGGCCCTGGCAGACCGGCTGCAGAAACACAAC
GlySerPheLysAspArgProLeuAlaAspArgLeuGlnLysHisAsn

241 CCTGGGAGGACGAGTATGAGAAGGCTGTGGaGAACCTTATCTACTCC
ProGlyGluAspGluTyrGluLysAlaValGluAsnPheIleTyrSer

289 TGGCTGGCTGCTGCGTGGCCACGTACGTCTTGGGCATCTGTGACCga
CysAlaGlyCysCysValAlaThrTyrValLeuGlyIleCysAspArg

337 CATAATGACAACATCATGCTGAAGACCACCTGGTCACATGTTCCACATC
HisAsnAspAsnIleMetLeuLysThrThrGlyHisMetPheHisIle

385 GACTTCGGC
AspPheGly

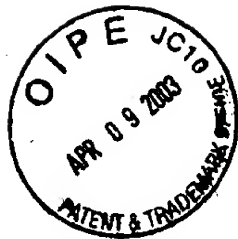


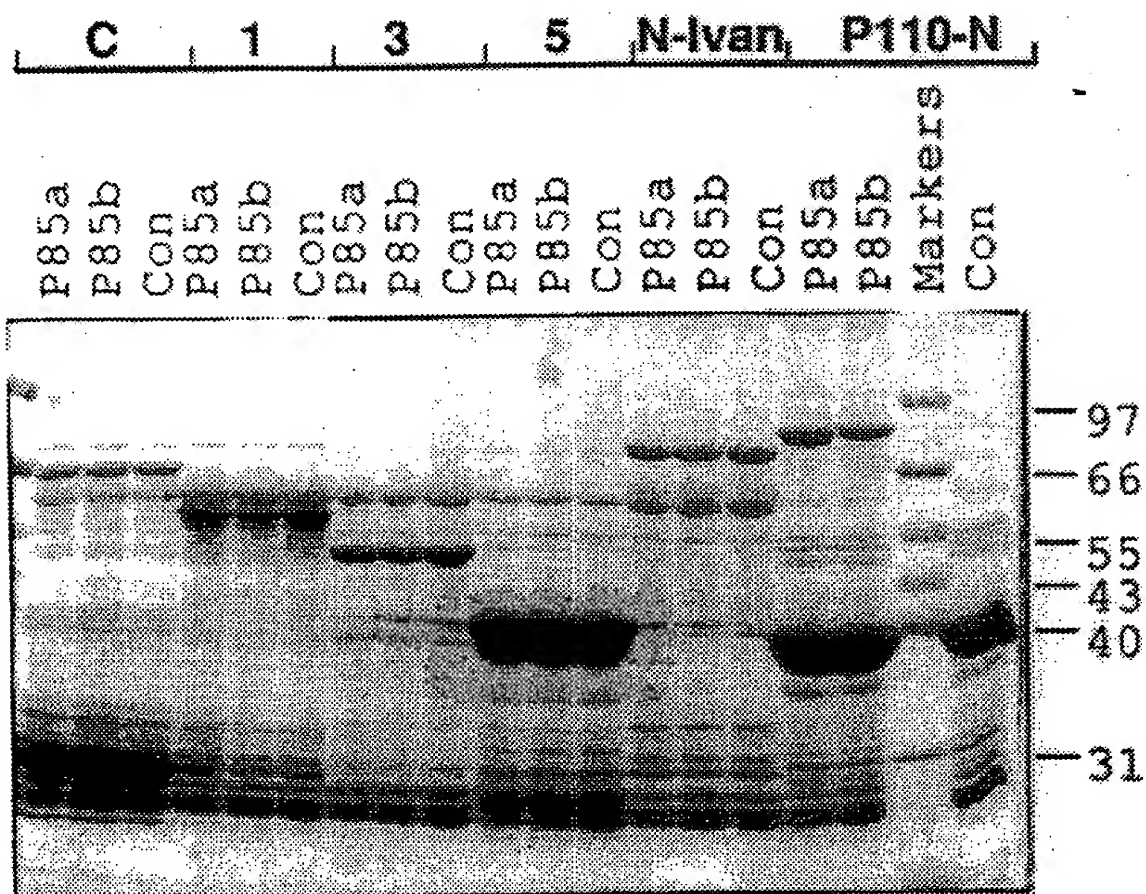
FIG. 22

1 50
vps34 GDDLRRQDqLvVQIIslMnellknEnvDLkLtPYkiLaTGpqeGaIEfIPN
PITR-c GDDLRRQDqLiLQIIslMdkllrkenLDLkLtPYkylLaTstkhGfmqfiqs
hump110 GDDLRRQDmLtLQIIriMeniwqnqgDLrMlPYgclsiGdcvGLIEvVrN
PITR-f GDDLRRQDmLtLQmIrimskiwwqEgLDmRMviFrcFSTGrGrGMVEmIPN
Consensus GDDLRRQD-L-LQII--M-----E-LDL---PY--L-TG---G-IE-I-N

51 100
vps34 dtlasilskyhGIlgY.....LklhypdenatlgvqgwvlDnFvkSCA
PITR-c vpvaevldegsIqnf.....FrkYapsenGpnngIsaevmDtYvkSCA
hump110 shtimqiqckgGlkGalqfnshLtLhqWlkdNkge.IydaaiDLftrSCA
PITR-f aetlrkiqvehGvtGs..fkdrpLadrIqkhNpgedeyekavEnFIySCA
Consensus -----GI-G-----L-----N-----I-----D-FV-SCA

101 133
vps34 GYCViTYILGVGDRHLDNlLvtpdGhFFHaDEG
PITR-c GYCViTYILGVGDRHLDNlLlktGkLFHIDEG
hump110 GYCVaTFILGIGDRHnsNiMvkddGqLFHIDEG
PITR-f GCCVaTYVLGICDRHdNiMlktGhMFHIDEG
Consensus GYCV-TYILG-GDRH-DN-----G-LFHIDEG

FIG. 23A



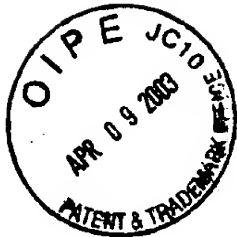
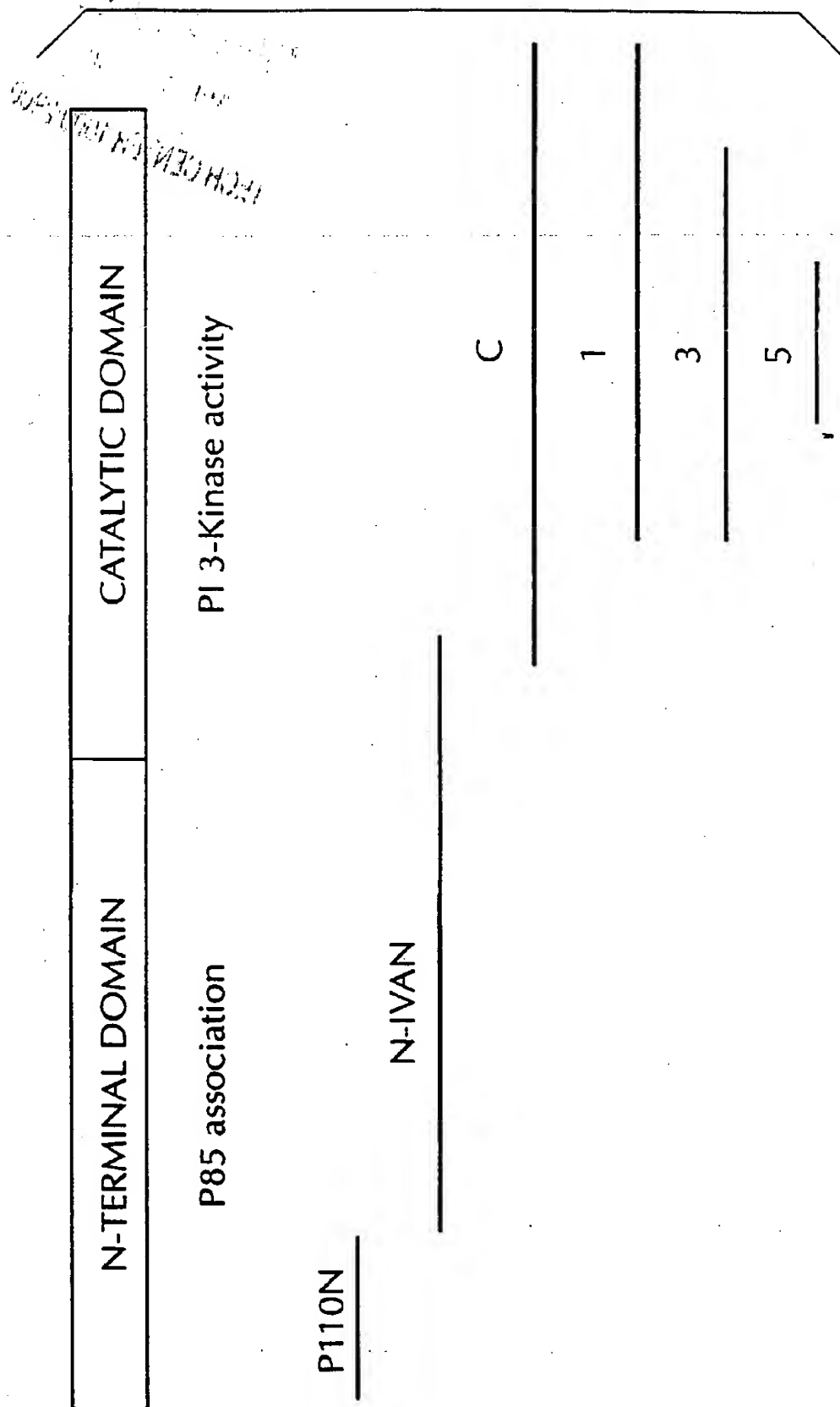


FIG. 23B



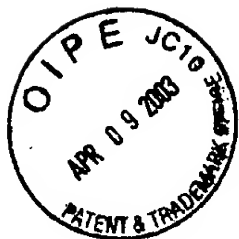
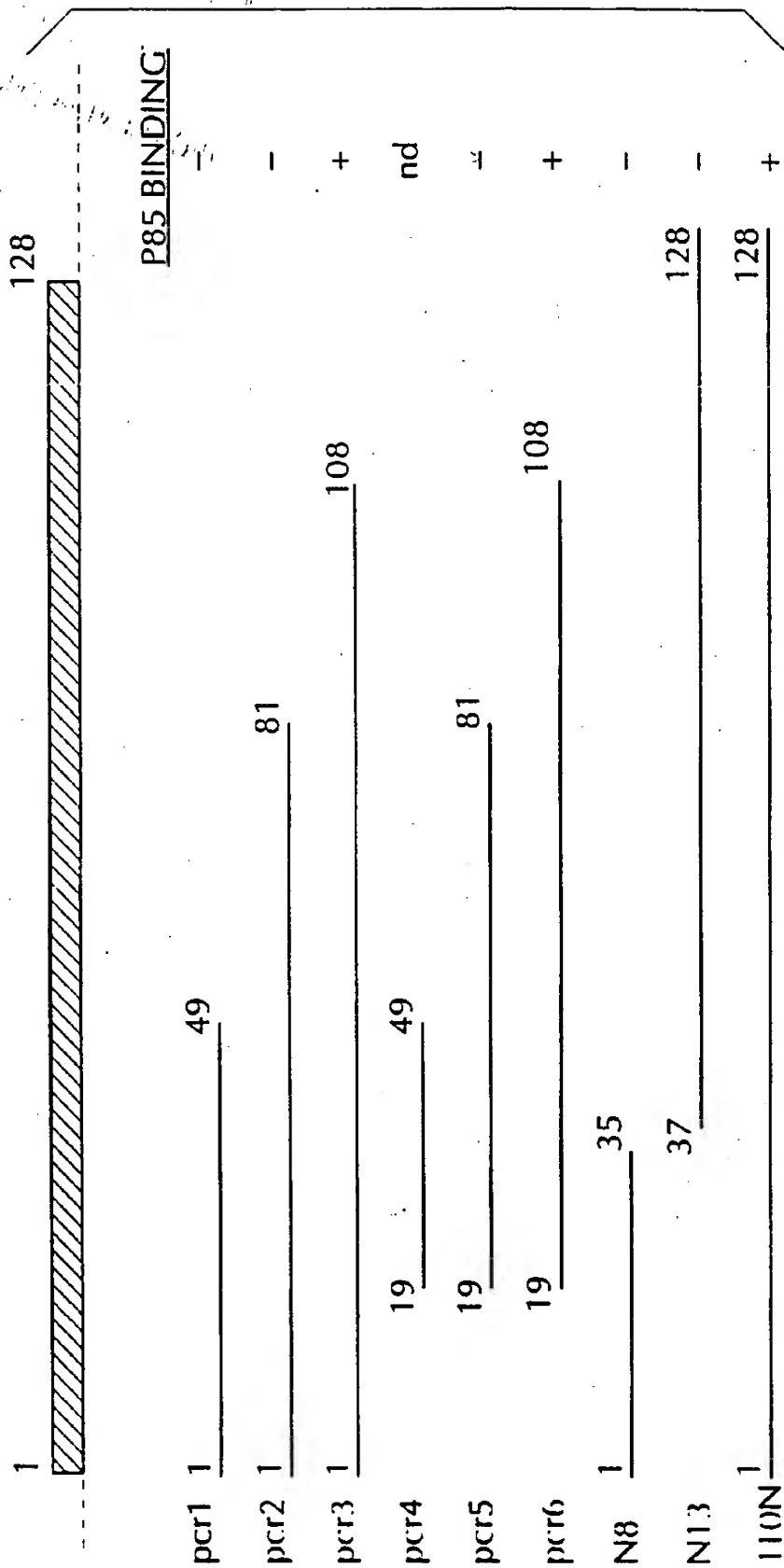


FIG. 24



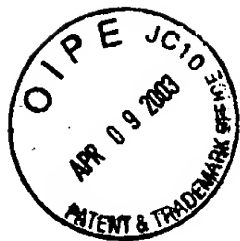
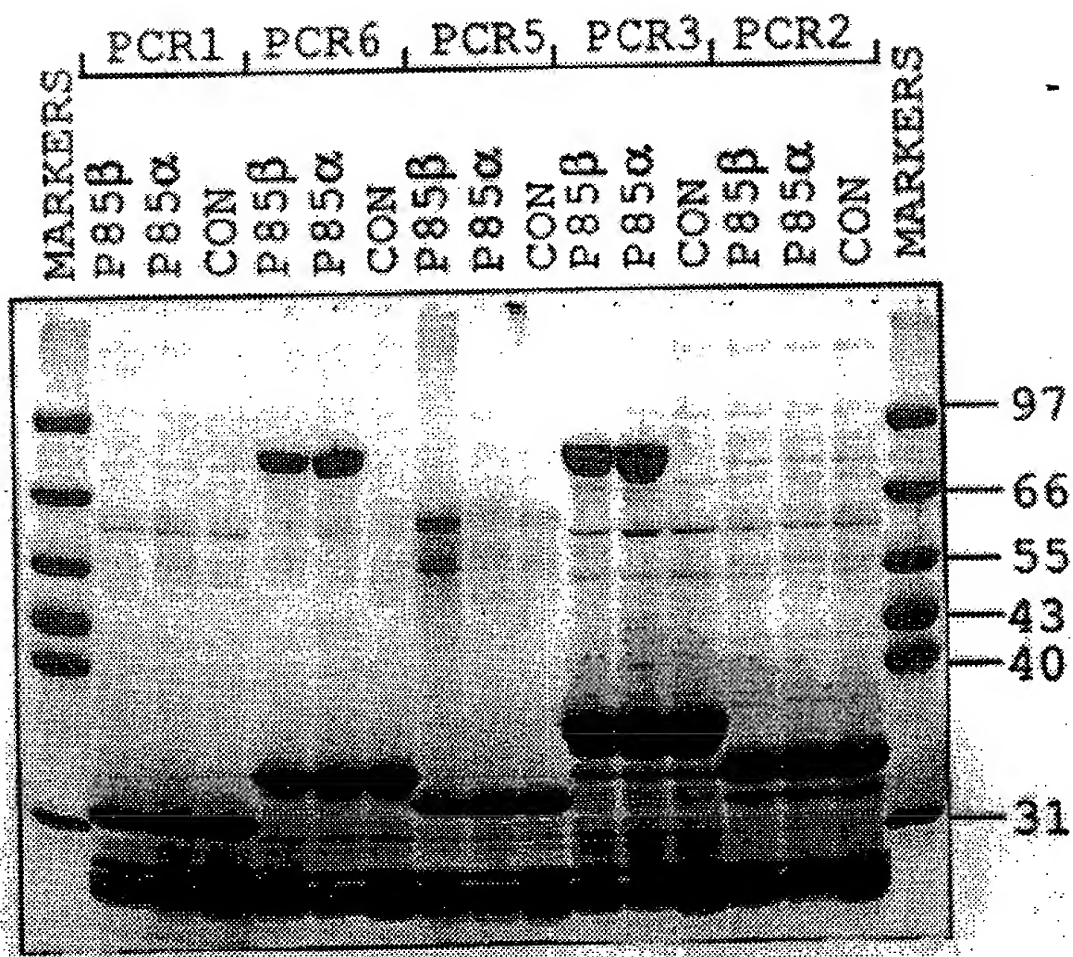


FIG. 25A



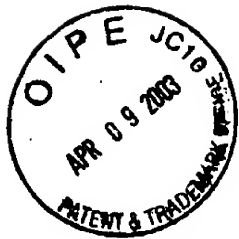


FIG. 25B

